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Result
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Maximum DB seq length: 200000000
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Perfect score:
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Maximum Match 100%
Listing first 45 s
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                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the score greater to and is derived
                                                                                        778
750.5
569.5
309
299
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      92.5
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90
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1: /cgn2_6/ptcdata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptcdata/1/pubpaa/USO7_NEW_PUB.pep:*

3: /cgn2_6/ptcdata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptcdata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptcdata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptcdata/1/pubpaa/USO8_NEW_PUB.pep:*

7: /cgn2_6/ptcdata/1/pubpaa/USO8_NEW_PUB.pep:*

9: /cgn2_6/ptcdata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*

10: /cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*

11: /cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*

12: /cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*

14: /cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*

16: /cgn2_6/ptcdata/1/pubpaa/USO0_PUBCOMB.pep:*

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16: /cgn2_6/ptcdata/1/pubpaa/USO0_NEW_PUB.pep:*

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17: /cgn2_6/ptcdata/1/pubpaa/USO0_NEW_PUB.pep:*

18: /cgn2_6/ptcdata/1/pubpaa/USO0_NEW_PUB.pep:*

19: /cgn2_6/ptcdata/1/pubpaa/USO0_NEW_PUB.pep:*

10: /cgn2_6/ptcdata/1/pubpaa/USO0_NEW_PUB.pep:*

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10: /cgn2_6/ptcdata/1/pubpaa/USO0_NEW_PUB.pep:*
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    100.0
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96.5
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-293-239-19
US-10-293-239-21
US-10-293-239-20
US-10-293-239-18
US-10-293-239-27
US-10-293-239-37
US-10-293-239-37
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             Sequence 17, Appl
Sequence 30, Appl
Sequence 19, Appl
Sequence 21, Appl
Sequence 20, Appl
Sequence 18, Appl
Sequence 22, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 181279
Sequence 181279
Sequence 117447, A
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Query Match Best Local S Matches 145 Qy 1 Db 1 Qy 61 Db 61 Db 61 Db 121	RESULT 1 US_10_293_239-1 GEQUENCE TY, Publication N GENERAL INFOR APPLICANT: APPLICANT: FILE REFEREN CURRENT EPLI CURRENT EPLI PRIOR_APPLICA CURRENT EPLI PRIOR_APPLICA CURRENT EPLI PRIOR_APPLI CURRENT EPLI FRI FRI FRI GRGANISM: US-10-293-239-1	25 25 26 27 28 33.5 29 31 30 31 31 32 32 33 31 32 32 33 34 35 36 37 38 38 39 31 31 31 32 32 33 34 35 36 36 37 38 38 38 38 38 38 38 38 38 38 38 38 38	
Similarity 100,0%; Score 778; DB 14; Length 145; Similarity 100,0%; Pred: No. 12-66; Similarity 100,0%; Pred: No. 12-66; Conservative 0; Mismatches 0; Indels 0; Gaps MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL	Application_US/102932 Application_US/102932 Application_US/102932 No.(US20030119043A1) RMATION: Tanner, Stephan Tanner, Stephan de la Chappelle, Alber VENTION: BAALC express NCE: 22727/04101 LICATION NUMBER: US/10 LICATION NUMBER	10.8 514 514 514 514 514 514 514 514 515 514 515 514 515 514 515 514 515 514 515 514 515 514 515 514 515 514 515 514 515 514 515 515	11.2 369 1 11.2 369 1 11.2 369 1 11.2 369 1 11.2 383 1 11.2 136 1 11.1 1342 1 11.1 342 1 11.1 342 1 11.1 468 1
*; SCOYE 778; DB 14; Length 145; *; Pred. No. 1e-66; 0; Mismatches 0; Indels 0; Gaps SWITRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDG	a diagnostic marker	12-363-154 137-963-168390 1457-761-12110 767-701-32315 437-963-147910 71-600-1170 72-701-57343 737-963-157852 424-599-242653 742-599-174991 742-599-174991 742-599-174991 742-599-174991 742-599-209325 742-599-209325 742-599-209325 742-599-209325 742-599-209325 742-599-209325 742-599-209325 742-599-209325 743-599-209325 743-599-10097 753-118	
0; Gaps 0; (GGLHSGMLEDGL 60 (GGLHSGMLEDGL 60	for acute leukemi	154, App e 168390, e 168390, e 12315, e 32315, e 147910, e 157853, e 1635491, e 69350, e 69350, e 69350, e 69350, e 62333, p e 242733, p e 242733, p e 242733, p e 6662, App e 190791, e 690971, e 6909711, e 690971, e 690971, e 6909711, e 69097111, e 69097111, e 69097111, e 690971111, e 690971111, e 6909711111, e 6909711111, e 6909711111111111111111111111111111111111	Sequence 26, Appl Sequence 84, Appl Sequence 149, Appl Sequence 4, Appli Sequence 32058, A Sequence 179100, Sequence 37779, A Sequence 914, App Sequence 134726, Sequence 134726, Sequence 71015, A

leukemia

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Sequence 30, Application US/10177390

Publication No. US20030143743A1

GENERAL INFORMATION:
APPLICANT: Schuler, Gerold
APPLICANT: Schuler, Gerold
APPLICANT: N.V. Antwerps Innovatiscentrum
TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
TITLE OF INVENTION: Polynucleotides by Electroporation
FILE REFERENCE: 021505wo/JH/ml
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT FILING DATE: 2002-06-20

NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 30
LENGTH: 145
TYPE: PRT
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APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REPERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/10293239 Publication No. US20030119043A1 GENERAL INFORMATION:
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                                                                                                                                               1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHS-----
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QCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAKEVTINVTDSIQQMDRSRRITKNCVN 145
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                                                                                                                       MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSVLEAEKS
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80.6%;
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                                                                               GMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET
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; Sequence 21, Application US/10293239
; Depurication No. US20030119043A1
; GENERAL INFORMATION;
; APPLICANT: Tanner, Stephan
; APPLICANT: de la Chapelle, Albert
; TITLE OF INVENTION BAALC expression as a diagnostic mar
; FILE REFERENCE: 22727/04101
; CURRENT APPLICATION NUMBER: US/10/293,239
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/348,210
; PRIOR APPLICATION NUMBER: US 60/348,210
; PRIOR FILING DATE: 2001-11-09
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; SEQ ID NO 20
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-239-20
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LENGTH: 149
TYPE: PRT
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                                                                                  Query Match
Best Local S
Matches 56
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APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
NUMBER OF SEQ ID NOS: 39
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SOFTWARE: PatentIn version 3.1
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                                                                                                         Local Similarity
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Local Similarity 75.7%;
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                    MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLED 58
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MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGCLEE 58
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                                                                                    Conservative
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                                                                                  Score 309; DB 14;
Pred. No. 4.6e-22;
1; Mismatches 1;
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RESULT 6

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US-10-293-239-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; P
Matches 54; Conservative 0;
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SEQ ID NO 18
LENGTH: 54
                                                                                                                                                                                         Sequence 37, Applica Publication No. US20 GENERAL INFORMATION:
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Best Local Similarity
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      APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR PILING DATE: 2001-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a
FILE REFERENCE: 22727/04101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
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APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727704101
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                        53,
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                                                                                                                                                                                                                                                                                                                                                  MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHS 53
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                                                                                                                                                                                                               Application US/10293239
No. US20030119043A1
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No. US20030119043A1
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.7%; Score 293; DB 14; Length 80 100.0%; Pred. No. 1.8e-20;
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100.0%; Pred. No. 2.9
tive 0; Mismatches
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 181279
LENGTU. 7.7
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APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 181279, Application US Publication No. US20040123343A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: unsure
LOCATION: (1)..(307)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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                                                                              ORGANISM: Oryza sativa
                                                                                                  TYPE: PRT
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                                                                                                                    LENGTH: 307
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Wu, Wei
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100.0%; Pred. No.
tive 0; Mismatci
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                                                                                                                                                                                      RESULT 12
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                                                                                                           Sequence 14107, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/10415147 Publication No. US20040043399A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 37; Conserv
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BAYER AG
TITLE OF INVENTION: REGULATION OF HUMAN INOSITOL POLYPHOSPHATE 5-PHOSPHATASE
FILE REFERENCE: LI0235Foreign Countries
CURRENT APPLICATION NUMBER: US/10/415,147
CURRENT FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 60/243,745
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2000-12-26
PRIOR FILING DATE: US 60/314,660
                                                                         APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 PRLT---TPTPTPTPPSSTPRLSLSSLRRLLTPPPRCLLTSHARRPPLQTHDRRRPLQSM 199
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                                                                                                                                                                                                                                                                                                                                                                                                                             12 EPRYYESWTRETESTWLTYTDSDAPP----SAAAPDSGPEAGGLHSGMLEDGLPS
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
                                                                                                                                                                                                                                            TQES
                                                                                                                                                                                                                                                                                 TTEA 110
                                                                                                                                                                                                                                                                                                                 N----QTVPPPLPKPPRSPSRSPSRSPNRSPCVPPAPEVALPRPVTQGAGPGKCPSPNLQ
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27.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 92.5;
Pred. No. 7;
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FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR FILING DATE: 2001-08-02

1 NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 14107

LENGTH: 670

TYPE: PRT
RESULT 14
US-09-910-600-26
; Sequence 26, Application US/09910600
; Publication No. US20030036631A1
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                                                                                                                                                                                                                                                                                            ; TYPE: PRT ; ORGANISM: Streptomyces avermitilis US-10-156-761-13447
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: INTERMA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JD 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSH
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                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13447
LENGTH: 219
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                      Query Match
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Best Local Similarity
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                  11.6%;
Local Similarity 33.9%;
es 20; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 AAPAEE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 GHRGEGMSPR------TNDSAPESDGGEQPPAGPEAGTAETGTPASATGT 59
                                                                                                                                                                  6 SRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGLPSNG
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ilarity 25.4%;
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Pred. No. 6;
14; Mismatches
                                                                                                                                                                                                                              Score 90; DB 14; Length 219; Pred. No. 1.9;
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APPLICANT: Birse et al.

TITLE OF INVENTION: 25 Human Prostate and Prostate Cancer Associated Proteins
FILE REFERENCE: PA002P1

CURRENT APPLICATION NUMBER: US/10/036,542

CURRENT APPLICATION NUMBER: PCT/US00/19666

PRIOR APPLICATION NUMBER: FCT/US00/19666

PRIOR FILLING DATE: 2000-07-20

PRIOR FILLING DATE: 1999-07-21

PRIOR APPLICATION NUMBER: 60/144,972

PRIOR APPLICATION NUMBER: 60/148,681

PRIOR FILLING DATE: 1999-08-13

PRIOR FILING DATE: 1999-08-13

PRIOR APPLICATION NUMBER: 60/149,173

PRIOR APPLICATION NUMBER: 60/158,004

PRIOR FILLING DATE: 1999-08-13

PRIOR FILLING DATE: 1999-08-13

PRIOR APPLICATION NUMBER: 60/158,004

PRIOR PILLING DATE: 1999-08-13

PRIOR APPLICATION NUMBER: 60/158,004

PRIOR FILLING DATE: 1999-08-13
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US-10-036-542-84
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Best Local S
Matches 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 84, Application US/10036542 Publication No. US20030083481A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 84
LENGTH: 369
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Best Local Similarity
Matches 33; Conserv
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APPLICANT: Longphre, Malinda
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APPLICANT: Whitney, Gena
TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
FILE REFERENCE: D0003NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/194,689 PRIOR FILING DATE: 2000-04-05
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                / Match 11.2%; Score 87.5; DI Local Similarity 25.9%; Pred. No. 6.2; Pees 28; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 CFKKRIEAIPQIDKYLKSSKYIAWPLQ---GWQATFGGGDHPPKSDLVPRGSPNSINVVP 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 TAGPLAQKRNQKATPNS--PRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQE 292
92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CGGSRADAI-----EPRYYESWTRETESTW-LTYTDSDAPPSA-----AAPDS---GP 46
SLSSGPL-----TQKQNGLQTTEAKRDAKRMPAKEVTINVTDSIQ 131
                                                       SSTSTSSSFPSSFPSSSSSSSSSSSCYPLIPS--TPEEVSADDETPNPPQ--SAQIACSSPS 95
                                                                                                           SDAPPSAAAPDSGPEAGGLHSGMLEDGLPSNGVPRS-TAPGGIPNPEKKTNCETQCPNPQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-04-05
                                                                                                                                                                                                                       DB 14; Length 369;
                                                                                                                                                                     48; Indels 13;
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Db 96 VVASLPLDQSDEGSSSQXEESPSTLQVLPDSESLPRSEIDEKVTDLVQ 143

Search completed: April 12, 2005, 16:03:42 Job time: 75.6667 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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RESULT 2
AAO19498
ID AAO1
XX AAO1
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Best Local Similarity
Matches 145; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      010 A00 2002
Claim 10; Page
                                                                 Diagnosis and therapy of tumors, specific expressed sequence tags blocking their expression.
                                                                                                                                                                                                           WPI; 2002-644836/70.
N-PSDB; AAL50100.
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   10pp; German
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Pred. No. 4e-70;
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                                                                                                  determining expression rates of
the unigene cluster, and subseq
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The present invention relates to the use of expressed sequence tags (BSTs), or variants, of the unigene cluster HS169395 (HS1), HS127144

The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down

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Matches 145;
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20-SEP-2001; 2001US-0323887P.
13-NOV-2001; 2001US-0350666P.
08-FEB-2002; 2002US-0355145P.
08-FEB-2002; 2002US-0355257P.
12-APR-2002; 2002US-0372246P.
                                                                New genes that are up-regulated or down-regulated in cancers, useful as markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
                                                                                                                        WPI; 2003-354600/33.
N-PSDB; ACC72796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HS2) and/or HS132793 (HS3) for diagnosis and therapy of tumours, in which their expression rates in tumour cells and/or lymph nodes are determined. The EST sequences are useful as prognostic markers of survival of cancer pattents (high levels of EST-related mRNA are associated with a poor prognosis, specifically correlated with development of metastasds); and for diagnosis and/or therapy of solid tumours, particularly of colon, stomach and breast. The present sequence is a variant of the HS1 protein shown in the exemplification of the
                                      Claim 12; Page 753; 767pp; English
                                                                                                                                                                     Zlotník
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
heart disease; atherosclerosis; endometriosis.
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ALIGNMENTS

RESULT-1 AAB95018 29-JUL-1999; 27-AUG-1999; 11-JAN-2000; 02-MAY-2000; 09-JUN-2000; 07-FEB-2001). EP1074617-A2 Human; primer; AAB95018 standard; 28-JUL-2000; 2000EP-00116126 Human protein sequence 26-JUN-2001 AAB95018; Homo sapiens (HELI-) HELIX RES INST. ; 99JP-00300253. ; 2000JP-00118776. ; 2000JP-00183767. ; 2000JP-00241899. (first entry) detection; diagnosis; antisense therapy; gene therapy. 99JP-00248036 protein; SEQ ID NO:16726 145 B

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end

Ota T, Ishii !

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Isogai T, Nishikawa T, , Sugiyama T, Wakamatsu

Hayashi K, S A, Nagai K,

Saito K, C, Otsuki

Yamamoto

WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length

Claim CDNAs.

8; SEQ ID NO 16726; 2537pp +

Sequence Listing; English

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RESULT 2
AAO19498
ID AAO1
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Best Local Similarity
Matches 145; Conserv
                                                                                                                         Diagnosis and therapy of tumors, specific expressed sequence tags blocking their expression.
                                                                                                                                                                                                                               WPI; 2002-644836/70.
N-PSDB; AAL50100.
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The present invention relates to the use of expressed sequence tags (ESTs), or variants, of the unigene cluster HS169395 (HS1), HS127144
                                                                            Claim 10; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HS1; variant; cancer; tumour; unigene cluster; cytostatic; metastasis; EST; expressed sequence tag; colon cancer; stomach cancer; breast cancer; HS169395; HS127144; HS2; HS132793; HS3.
                                                                                                                                                                                                                                                                                                                                                                                                        26-JAN-2001; 2001DE-01003694
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                                                                       5; 10pp; German
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the unigene cluster, and subseq
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The present invention describes an isolated nucleic comprises the sequence of any of the genes that are

acid molecule, which up-regulated or down

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RESULT 3
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20-SEP-2001; 2001US-0323887P.
13-NOV-2001; 2001US-0350666P.
08-FEB-2002; 2002US-0355145P.
08-PEB-2002; 2002US-0355257P.
12-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HS2) and/or HS132793 (HS3) for diagnosis and therapy of tumours, in which their expression rates in tumour cells and/or lymph nodes are determined. The BST sequences are useful as prognostic markers of survival of cancer patients (high levels of EST-related mRNA are associated with a poor prognosis, specifically correlated with development of metastases); and for diagnosis and/or therapy of solid tumours, particularly of colon, stomach and breast. The present sequer is a variant of the HS1 protein shown in the exemplification of the
                                   Claim 12; Page 753; 767pp; English
                                                           New genes that are up-regulated or down-regulated in cancers, useful as markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
                                                                                                                   N-PSDB;
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Zlotnik
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                                                                                                                                                                     Gish KC,
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                                                                                                                                                                     Mack DH,
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CC regulated in specific cancers (e.g. about 1031 genes up-regulated in CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer CC related gene nucleotide sequences which encode the proteins given in CC ABR58521 to ABR5879. Also described: (1) determining the presence or CC comprising a nucleic acid molecule described above; (2) an expression vector CC comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a CC patient by administering to the patient the antibody above; and (7) a CC drug screening assay. The nucleic acid is useful as diagnostic markers or CC therapeutic targets. In particular, the nucleic acid is useful for CC therapeutic targets. In particular, the nucleic acid is useful for CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in CC carefulariae.
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Best Local Similarity 100
Matches 145; Conservative
                               Tang TY, Zhang J,
Zhou P, Ghosh M,
                                                                                                                                                                                                                                                                                                                             ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoasgulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                       Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                 24-SEP-2002; 2002WO-US030474.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human novel polypeptide sequence, SEQ ID NO:1882.
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Wang D,
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100.0%; Pred. No. 4e:
tive 0; Mismatches
                               Xue AJ,
Ma Y, A
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Claim
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N-PSDB; ADC30829.
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                                                                                                                                                                                                   SEQ ID NO 1882; 1185pp; English
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The invention relates to 971 novel human cDNA sequences (ADC29919-CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The cinvention also relates to nucleic acid sequences over 99% identical with CC the novel human cDNAs. The invention additionally encompasses expression CC vectors and host cells comprising a nucleic acid of the invention; the CC recombinant production of a polypeptide of the invention; an antibody CC against a polypeptide of the invention; and methods of polypeptide of the invention; and methods of polypeptide of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The CC invention further discloses methods of perventing, treating or amelical condition; kits comprising polynuclectide probes and/or monoclonal antibodies for carrying out the methods of the expression or activity of the polynuclectide and/or polypeptide, and 767 CC contig sequences corresponding to the cDNA sequences of the invention are cuseful in diagnostics, drug screening, forensics, gene mapping, in the CC identification of mutations responsible for genetic disorders or other CC traits, for assessing biodiversity, and in producting many other types of CC data and products dependent on DNA and amino acid sequences. They are CC disease and other neurodegenerative diseases, anaemia, platelet CC disease, and in the recombinant production of a protein. The polypeptides or CC cancer. The nucleic acids may also be used as hybridisation probes or CC cancer. The nucleic acids may also be used as hybridisation probes or CC cancer. The nucleic acids may also be used as hybridisation probes or CC cancer. The nucleic acids may also be used as hybridisation probes or CC cancer. The presents sequence of the protection. Note: The polypeptide are also useful in generating antibodies, as molecular weight markers, can also be also be also be also be acids and are represents a specifically conditions. The present directly from WIPO at Seguence 145 AΑ;

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Best Local Similarity
                                                                                                                                                           Matches 145;
121 EVTINVTDSIQQMDRSRRITKNCVN 145
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                                                 61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
                                                                                                               1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                             MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                          Conservative
                                                                                                                                                                          100.0%; Score 778; DB 7
100.0%; Pred. No. 4e-70;
                                : PNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK
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AC ADM4
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AC ADM4
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DT 03-J
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DE Brai
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KW acut
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                             Brain and Acute Leukemia, Cytoplasmic alternate protein #1.
acute myelogenous leukemia; gene expression; BAALC
                                                                                         ADM46959;
                                                                                                                 ADM46959 standard; protein;
                                                        (first entry)
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RESULT 6
ADO48475
ID ADO4
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                               Matches 145;
                            PTH responsive genetransgenic animal;
                                                                          Human PTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of characterizing acute myelogenous leukemia (AMI) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
   Homo sapiens
                                                                                                     12-AUG-2004
                                                                                                                                                            ADO48475 standard; protein; 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 17; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAALC transcripts in cells obtained from the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Characterizing acute or chronic myelogenous leukemia, c in a patient comprises assaying for the overexpression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia; Cytoplasmic; exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-2001; 2001US-0348210P
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                                                                                                                                                                                                                                                                                              PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK
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                                                                        responsive
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                    (first entry)
                         gene; PAIGB; bone-forming; bone; bone density modulation;
mal; osteopathic; gene therapy; osteoporosis; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                       gene protein
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Pred. No.
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                                                                                                                                                                                                  Matches 145;
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid fragment encoding a PAIGB polypeptide, useful preparing a composition for diagnosing, treating or preventing related disorders, e.g., osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; SEQ ID NO 4; 169pp; English
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                                                                                                                                                                                                                       Local Similarity
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EVTINVTDSIQQMDRSRRITKNCVN 145
                                                                         PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK 120
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                                     PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK
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EVTINUTOSIQQMDRSRRITKNCVN 145

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                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-NOV-2001; 2001US-0348210P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method of characterizing acute myelogenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID
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                                         QCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAKEVTINVTDSIQQMDRSRRITKNCVN
                                                                                                                                                                                                                                                                               MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHS------
QCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAKEVTINVTDSIQQMDRSRRITKNCVN
                                                                                                                       KIKAPTDSVSDEGLFSASKMAPLAVFSHGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET
                                                                                                                                                                                                                                               MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSVLEAEKS
                                                                                                                                                                                                                                                                                                                                                                       Conservative
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80.6%;
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RESULT 8
ADO48479
ID ADO4
The invention relates to a novel PTH responsive gene (PAIGB) fragment CC construct comprising the isolated nucleic acid fragment operatively (CC linked to suitable regulatory sequences; a host cell transformed with the CC chimeric construct; a vector comprising the public acid fragment; obtaining a nucleic acid fragment encoding the polypeptide; a method for CC chaining a polypeptide; detecting the presence of the nucleic acid fragment; and antibody that specifically binds to one or more epitopes of CC a PAIGB polypeptide; a composition for regulating bone-forming activity (C) in a mammal comprising the nucleic acid fragment, polypeptide; a method for CC determining whether an agent altering expression of PAIGB mRNA; CC determining agents for effectiveness in altering expression of the nucleic acid fragment; subject; identifying polypeptides of a bone related disorders; evaluating the effectiveness in altering expression of the bone related CC disorder in a subject; identifying polypeptides capable of binding to CC pAIGB, monitoring the effectiveness of treatment of a subject with a bone CC paigness in altering expression of the muleic canimals and a second group of control canimals composed of the transgenic animal and a second group of control canimals, studying bone mass determinants; studying the modulation of bone mass; studying an effect of PAIGB on bone disorders; identifying not whether an agent which a slinked to an activation domain cC construct comprising multiple copies of DNA binding elements linked to a linked to a material promoter which is linked to paign whether an agent which is linked to an activation domain composition of paign generate linked to a construct observation domain of paign specifical inducer, transcription of paign generate linked to a construct observation domain which is linked to an activation of bone construct disorders by gene therapy. The nucleic acid is useful in celebrating a composition of the may be construct acid disorders, e.g., osteoporosis. This sequence represents
              New nucleic acid fragment encoding a PAIGB polypeptide, useful in preparing a composition for diagnosing, treating or preventing bone
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N-PSDB; ADO48478.
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related disorders,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADO48479;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-NOV-2003; 2003WO-US035655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; SEQ ID NO 8; 169pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  responsive gene protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 animal; osteopathic; gene therapy; osteoporosis; mouse,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Babij P,
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cc encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively cc linked to suitable regulatory sequences; a host cell transformed with the chimeric construct; a vector comprising the nucleic acid fragment; containing a nucleic acid fragment encoding the polypeptide; a method for containing a polypeptide; detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of cc a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody a magent that alters the expression of PAIGB gene or polypeptide; cc determining whether an agent alters the expression of PAIGB mRNA; cc screening agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related cd isorders; evaluating the efficacy of a treatment of a bone related cd isorders; monitoring the effectiveness of treatment of a bone related to PAIGB; monitoring the effectiveness of treatment of a bone related construction.
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                                                                                                                                                                                                                                                                                                                                                     New nucleic acid fragment encoding a PAIGB preparing a composition for diagnosing, tre related disorders, e.g., osteoporosis.
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                                                                                                                                                                                                                                                                                                                        Claim 9; SEQ ID NO 2; 169pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat PTH responsive gene protein.
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DB; ADO48472.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 145
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                                                                                                                                                                                                                                                                                       a novel PTH responsive gene (PAIGB) fragment
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Pred. No. '
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                                                                                                                                                                                                                                                                                                                                                                         IGB polypeptide, useful in treating or preventing bone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                           09-NOV-2001; 2001US-0348210P
                                                                                                                                                                                                                   15-MAY-2003.
                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      Cytoplasmic; exon.
                                                                                                                                                                                                                                                                                                                                                                                                                     acute myelogenous leukemia; gene expression; BAALC; chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brain and Acute Leukemia, Cytoplasmic alternate protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUN-2004
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                                                                    Tanner SM,
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                                                                                                                                                                               12-NOV-2002; 2002WO-US036375
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                                                                    De La Chapell A;
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                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                           /note= "encoded by GCS"
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WPI; 2003-441564/41. N-PSDB; ADM46955.

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Best Local Sim
Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                                 New polypeptide human dioxygenase 10.12 and polynucleotides encoding polypeptide, useful for treating various diseases, such as malignant tumors, inflammations, immunological diseases, hemopathy and HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 149
                         Claim 1; SEQ ID NO 2; 33pp; Chinese.
                                                                                                                                                                                                                                                                           17-APR-2002
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                                                                                                                          N-PSDB;
                                                                                                                                                                                                                     29-SEP-2000; 2000CN-00125495
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                                                                                                                                                                                                                                                                                                                                                                         Human;
                                                                                                                                                                                                                                                                                                                                                                                                 Human dioxygenase 10.12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QCPNPQSLSSGPLTQKQNGLQTTE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIKAPTDSVSDEGLFSASKMAPLAVFSHGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QCPNPQSLSSGPLTQKQNGLQTTE 144
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                                                                                                                                                                                                                                                                                                                                                         dioxygenase 10.12; malignant tumour; inflammation; disease; haemopathy; HIV infection.
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                                                                                                                                                                                          BIODOOR GENE DEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 569.5; DB 7
Pred. No. 4.2e-49;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₹
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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The

present invention

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RESULT 12
ADM46962
ID ADM46
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Matches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombination process to produce the polypeptide and antagonist age the polypeptide. The present invention also discloses the method of applying the polypeptide in treating various diseases, such as maltumours, inflammations, immunological diseases, haemopathy and HIV infection. The present sequence is the human dioxygenase 10.12.
                       overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative
                                                                                            The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one more BAALC transcripts in cells obtained from the patient, where an
                                                                                                                                                                             Characterizing acute or chronic myelogenous leukemia, c in a patient comprises assaying for the overexpression BAALC transcripts in cells obtained from the patient.
                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic; exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acute myelogenous leukemia; gene expression; BAALC chronic myelogenous leukemia; prostate cancer; Brai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brain and Acute Leukemia, Cytoplasmic alternate protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADM46962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADM46962 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dioxygenase 10.12, polynucleotides encoding this polypeptide, a
                                                                                                                                                    Disclosure; SEQ ID NO 20; 78pp; English.
                                                                                                                                                                                                                                                                                Tanner SM,
                                                                                                                                                                                                                                                                                                                                        09-NOV-2001; 2001US-0348210P
                                                                                                                                                                                                                                                                                                                                                                  12-NOV-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                            (OHIS ) UNIV OHIO STATE RES FOUND
                                                                                                                                                                                                                                                    2003-441564/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 GPEAGGLHSGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80;
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                                                                                                                                                                                                                                       ADM46954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQTTEAKRDAKRMPAKEVTINVTDSIQQMDRSRRITKNCVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOTTEAKRDAKRMPAKEVTINVTDSIQQMDRSRRITKNCVN
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           consisting
                                                                                                                                                                                                                                                                                De La Chapell A;
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                                                                                                                                                                                                                                                                                                                                                                  2002WO-US036375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
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79.2%;
             of exons
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Pred. No. 7.5e-33;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCS"
              and
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                                                                                                                                                                                              or prostate
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Best Local
                                                                                                                                  The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BALIC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BALIC overexpression. This sequence corresponds to a BALIC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                                                                             Sequence 54
                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 18; 78pp; English.
                                                                                                                                                                                                                                                                                                          Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-NOV-2002; 2002WO-US036375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acute myelogenous leukemia; gene expression; BAALC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brain and Acute Leukemia, Cytoplasmic alternate protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003040347-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytoplasmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM46960 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                          (OHIS ) UNIV OHIO STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                    2003-441564/41.
                                                      54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLED 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56
                                                                    Similarity
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                          MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73
MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGCLEE 58
                                                                                                                                                                                                                                                                                                                                                                                                             De La Chapell A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AΑ;
                                                       Conservative
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100.0%;
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                                                                                Score 299;
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Pred. No. 2.9e-23;
                                                                    Pred. No.
                                                       Mismatches
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                                                                    2e-22;
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CC encoding a polyapetide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively construct; a vector comprising the mucleic acid fragment operatively containing a nucleic acid fragment encoding the mucleic acid fragment; construct; a vector comprising the nucleic acid fragment; cobtaining a nucleic acid fragment encoding the polyapetide; a method for cobtaining a nucleic acid fragment encoding the polyapetide; a method for cobtaining a polyapetide; detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of care a PAIGB polyapetide; a composition for regulating bone-forming activity cin a mammal comprising the nucleic acid fragment, polyapetide or antibody determining agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related condisorders; evaluating the effectiveness in treating bone related condisorders; evaluating the effectiveness of treatment of a bone related condisorders; evaluating the effectiveness of treatment of a bone related condition; a transgenic animal comprising a first group of control condition; a transgenic animal comprising a first group of control condition; a treating bone related disorders; studying bone mass determinants; studying the modulation of bone mass; studying an effect of PAIGB on bone disorders; identifying an agent of the transgenic animal and a second group of control construct comprising multiple copies of DNA binding elements linked to a paid bone related disorders; but the struct of paids of bone and a linked to a DNA binding domain which is linked to an activation domain condition of paids gene the paids of condition of paids gene is induced. The PAIGB condition of paids gene is induced. The PAIGB condition of paids gene is induced. The PAIGB condition of paids of the nucleic acid is useful in ceptated disorders by gene therapy. The prut responsive gene may be conditioned in the paid of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; SEQ ID NO 6; 169pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid fragment encoding a PAIGB polypeptide, useful preparing a composition for diagnosing, treating or preventing related disorders, e.g., osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel PTH responsive gene (PAIGB) fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-2002; 2002US-0425532P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PTH responsive gene protein exon 2 splice variant
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Matches 53
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Best Local Similarity
                                                                                                                                             The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                                                                                                                                                                                                                                                                                         Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                                                                                    Sequence 80 AA;
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-441564/41.
N-PSDB; ADM46956.
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                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 22; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Tanner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytoplasmic; exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acute myelogenous leukemia; gene expression; BAALC; chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brain and Acute Leukemia, Cytoplasmic alternate protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADM46964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADM46964 standard; protein; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OHIS ) UNIV OHIO STATE RES FOUND
                                                        y Match
37.7%; Sc
Local Similarity 100.0%; p
hes 53; Conservative 0;
SM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGCGGSRADAIEPRYYESWIRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                    De La Chapell A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "encoded by GCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.4%; Score 299; DB 8; Length 54; 100.0%; Pred. No. 2e-22;
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                                                          Score 293; DB 7; ]; Pred. No. 1.4e-21; 0; Mismatches 0;
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Job time : 105.667 secs

Search completed: April 12, 2005, 15:37:18

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53

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Title:
Perfect score:
Sequence:
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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A Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2001s:*
4: geneseqp2001s:*
5: geneseqp2003s:*
6: geneseqp2003bs:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                               2105692 seqs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-705-716A-2
767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	9,	ۍ.	4	ω	2	1	NO.	Result	•
83.5	84	84	87.5	87.5	89	92.5	99	140	272	278	278	288	294	335.5	473.5	617.5	645	645	645	645	645	645	746	767	Score	•	
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AAE25052	ADA36828	ABU17344	ABG15607	ABG09899	ADO48482	AAR13456	ADM46977	ADM46979	ADM46964	ADO48477	ADM46960	ADM46962	ADO48481	ADQ81902	ADM46963	ADM46961	ADO48475	ADM46959	ADC31800	ABR58646	AAO19498	AAB95018	ADO48479	ADO48473	ID		
	Ada36828 Acinetoba	Abul7344 Protein e	Abg15607 Novel hum		Ado48482 PTH respo	Aar13456 Duffy rec	Adm46977 Brain and	Adm46979 Brain and	Adm46964 Brain and	Human	Adm46960 Brain and	Adm46962 Brain and			Brain	Adm46961 Brain and	Ado48475 Human PTH	Adm46959 Brain and	Adc31800 Human nov	Abr58646 Human can	Aaol9498 HS1 prote	Aab95018 Human pro	Ado48479 Mouse PTH	ĊŤ	Description		

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The enco cong link link link link link link link link	WO20040 27-WAY- 10-NOV- 12-NOV- (AMHP) Robinso WPI; 20 N-PSDB; New nuc prepari	444	0 2 2 0 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
laim 9; SEC ne invention ncoding a property of nonstruct construct construct con inked to service con interior con otaining a notaining a ragment; ar PAIGB poly n a mammal an agent to etermining	WO2004044152- 27-MAY-2004. 10-NOV-2003; 12-NOV-2002; (AMHP) WYETH Robinson JA, WPI; 2004-420 N-PSDB; ADO48 New nucleic a preparing a crelated disor	1 H M M M M	81.5 81.5 81.5 81.5 81.5 81.5 80.5 80.5 79.5 79.5 80.5
on repolypomprilitabilit	\$2-A2. 1. 2. 2003WO- 2. 2002US- 2. 2002US- 2. 2002US- 2. 2002US- 3. Stojan 3. Stojan 3. 20029/39. 48472. 3. acid fra 4. acid fra 4. acid fra 5. acid fra 6. acid	standard;];;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	11111111111111111111111111111111111111
NO 2; 169 lates to eptide. T sing the la regula ct; a vec eic acid ejectide; ibody that ide; a co rising the ran aglers the	2003WO-US035655. 2002US-0425532P. H. Stojanovic-Susulic 0299/39. 8472. acid fragment encodi accomposition for diag rders, e.g., osteopo	pro gen gen	1433 600 600 852 872 886 986 975 275 275 275 286 286 286 286 305 305 305
o a n The le 180 llator d fraa det hat s compo the n agent	og - Su 32 56 5	in; (y) prot	5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
novel PTH rese invention for solated nuclestory sequences, or comprising the parectifically position for a nucleic acid expression of alters the thing the position for a nucleic acid expression of alters the	V, V, ng a nosir rosis	ALIGNMENTS try) te protein. e protein. aligh; bone-forming; eopathic; gene ther	ABP35624 AAB14866 ADJ70139 AAM40296 AAM42081 AAM42081 AAM42081 AAM42082 AAM42082 AAM42082 AAM42082 ABC31379 ABC31379 ABC31379 ABC31379 ABC31316 ABC33316 ABC333
2; 169pp; English. tes to a novel PTH responsive gene (PAIGB) fragment tide. The invention further comprises: a chimeric ng the isolated nucleic acid fragment operatively regulatory sequences; a host cell transformed with the a vector comprising the nucleic acid fragment; c acid fragment encoding the polypeptide; a method for ptide; detecting the presence of the nucleic acid ody that specifically binds to one or more epitopes of a composition for regulating bone-forming activity sing the nucleic acid fragment, polypeptide or antibody ters the expression of PAIGB gene or polypeptide; r an agent alters the expression of PAIGB mRNA;	Babij P, Murrills RJ; PAIGB polypeptide, useful in g, treating or preventing bone	A. A. forming; bone; bone density modulation; ene therapy; osteoporosis; rat.	Abp35624 Fungal ZB Aae14866 S. clavul Adj70139 Human hea Adm40296 Human pol Aam40295 Human pol Aam40291 Human pol Aam42081 Human pol Aam42082 Human pol Adm42082 Human pol Adm42082 Human pol Adm42082 Human pol Adm20824 Antagonis Aau31506 Novel hum Abg21379 Novel hum Abg21379 Novel hum Abg15431 Novel hum Aay00097 Enterococ Abp43316 E faecali Abu13594 Enterococ Aay00096 Enterococ Aay00096 Enterococ Abp43315 E faecali Abu13594 Enterococ

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC screening agents for effectiveness in altering expression of the nucleic coid fragment; screening for agents useful for treating bone related CC disorders; evaluating the efficacy of a treatment of a bone related CC disorder in a subject; identifying polypeptides capable of binding to CC PAIGB; monitoring the effectiveness of treatment of a subject with a bone CC related agent; a transgenic animal comprising the DNA; an animal model CC for the study of bone density modulation comprising a first group of CC animals composed of the transgenic animal and a second group of control animals; studying bone mass determinants; studying the modulation of bone CC mass; studying bone mass determinants; studying the modulation of bone CC for treating bone related disorders; identifying an agent CC two constructs, the first construct formprising a ligand binding domain CC linked to a DNA binding domain which is linked to an activation domain CC all of which expression is driven by a constitutive promoter, the second CC construct comprising multiple copies of DNA binding elements linked to a CC construct comprising multiple copies of DNA binding elements linked to a CC construct comprising multiple copies of DNA, where upon the addition of chemical inducer, transcription of PAIGB gene is induced. The PAIGB colymucleotide has osteopathic activity. The PTH responsive gene may be considered disorders by gene therapy. The nucleic acid is useful in preparing a composition for diagnosing, treating on preventing bone created disorders, e.g., osteoporosis. This sequence represents a PTH cresponsive gene protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
N-PSDB; ADO48478
                WPI; 2004-420299/39
                                                    Robinson JA, Stojanovic-Susulic V,
                                                                                                                                                                                                                                                    WO2004044152-A2
                                                                                                                                                                                                                                                                                                                                               PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                          Mouse PTH responsive gene protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADO48479 standard; protein; 145
                                                                                                                                 12-NOV-2002; 2002US-0425532P
                                                                                                                                                                     10-NOV-2003; 2003WO-US035655
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                                                                                             HIBAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSNGVLRPAAPGGIANPEKKWNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGCGGGRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP
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Pred. No. 4.1e-76;
                                                    Babij P,
                                                      Murrills RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 145;
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AAB95018 ID AABS

AAB95018 standard;

protein;

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121 EVAISVTENIRQMDRSKRVTKNCIN 145

EVAINVTENIROMDRSKRVTKNCIN 145

XXXXXXXX

26-JUN-2001 AAB95018;

(first entry)

Human; primer; detection; diagnosis; antisense therapy; gene therapy.

Human protein sequence SEQ ID NO:16726.

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61 SSNGYLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR 120

SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAR

MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP

MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL

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61

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44 سر Matches 141;

Conservative

Query Match Best Local Similarity

97.3%; 97.2%;

Score 746; DB 8; Pred. No. 8.4e-74; Mismatches

Length 145; Indels

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The invention relates to a novel PTH responsive gene (PAIGB) fragment CC encoding a polypeptide. The invention further comprises: a chimmeric construct comprising the isolated nucleic acid fragment operatively CC linked to suitable regulatory sequences; a host cell transformed with the C chimmeric construct; a vector comprising the pulypeptide; acid fragment construct; a vector comprising the pulypeptide; acid fragment encoding the pulypeptide; amethod for C chaining a polypeptide; a composition for regulating bone or more epicopes of C a PAIGB polypeptide; a composition for regulating bone-forming activity; in a mammal comprising the mucleic acid fragment, polypeptide or antibody C; an agent that alters the expression of PAIGB gene or polypeptide; determining whether an agent alters the expression of paids many c cacid fragment; soreening for agents useful for treating bone related C disorders; evaluating the effectiveness in altering expression of the nucleic C acid fragment; soreening for agents useful for treating bone related C disorders; evaluating the effectiveness of treatment of a subject with a bone C pAIGB, monitoring the effectiveness of treatment of a subject with a bone C paids, monitoring the effectiveness of treatment of a subject with a bone C mass; studying bone mass determinants; studying the modulation comprising a first group of control C mass; studying bone mass determinants; studying the modulation of bone mass; studying bone related disorders; identifying whether an agent which has bone forming activity; and a stably transfected cell line comprising comprising multiple copies of DNA binding elements linked to a DNA binding domain which is linked to an activation domain C linked to a DNA binding domain which is linked to an activation domain c playmucleotide has osteopathic activity. The pTH responsive gene may be constituted as osteopathic activity. The process of the addition of classed to treat disorders by gene therapy. The nucleic acid is useful in useful in useful disorders, e.g., o
Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preparing a composition for diagnosis: related disorders, e.g., osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid fragment encoding a PAIGB polypeptide, useful in preparing a composition for diagnosing, treating or preventing bone
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                                                                                                                                                                                                                                                                                                    complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide or polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises a 1'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence, 3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human amino acid sequences; and AAH13639 to AAH13632 represent
                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                            Matches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; SEQ ID NO 16726; 2537pp + Sequence Listing; English
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Sugiyama
                                 EVAISVTENIROMDRSKRVTKNCIN 145
                                                                                  SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR 120
                                                                                                                                               MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP
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PSNGVPRSTAPGGI PNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK
                                                                                                                              MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
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; 2000JP-00118776.
; 2000JP-00183767.
; 2000JP-00241899.
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T, Wakamatsu
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Pred. No. 1.2e-62;
                                                                                                                                                                                            Mismatches
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A, Naga
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C, Otsuki
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RESULT 4 AAO19498

RESULT 5
ABR58646
ID ABR5
XX
AC ABR5
XX
DT 09-J

ABR58646 standard;

protein;

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ABR58646;

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Best Local S
Matches 121
                                                                                                                                                                                                                                                                       The present invention relates to the use of expressed sequence tags (BSTB), or variants, of the unigene cluster HS169395 (HS1), HS127144 (HS2) and/or HS132793 (HS3) for diagnosis and therapy of tumours, in which their expression rates in tumour cells and/or lymph nodes are determined. The EST sequences are useful as prognostic markers of survival of cancer patients (high levels of EST-related mRNA are associated with a poor prognosis, specifically correlated with development of metastases); and for diagnosis and/or therapy of solid tumours, particularly of colon, stomach and breast. The present sequents as a variant of the HS1 protein shown in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosis and therapy of tumors, specific expressed sequence tags blocking their expression.
                                                                                                                                                                                                                                Sequence 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAL50100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brett D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HS1; variant; cancer; tumour; unigene cluster; cytostatic; EST; expressed sequence tag; colon cancer; stomach cancer; HS169395; HS127144; HS2; HS132793; HS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JAN-2001; 2001DE-01003694.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HS1 protein variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAO19498 standard; protein; 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JAN-2001; 2001DE-01003694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
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 121
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                                                                           61 SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR
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                                                                                                                              1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP
                                                                                                                                                                                      Similarity
EVTINVIDSICOMDRSRRITKNCVN 145
                EVAISVTENIRQMDRSKRVTKNCIN
                                                       PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK
                                                                                                               MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 5; 10pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kemmner W;
                                                                                                                                                                          Conservative
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                                                                                                                                                                                      84.1%;
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                                                                                                                                                                       Score 645; DB 5;
Pred. No. 1.2e-62;
0; Mismatches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by determining expression rates of of the unigene cluster, and subsequently
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breast cancer;
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                                                                                                                                                                                                                                                               comprises the sequence of any of the genes that are up-regulated in specific cancers (e.g. about 1031 genes up-regulated in acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer related gene nucleotide sequences which encode the proteins given in ABR58521 to ABR58709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a drug screening assay. The nucleic acid is useful as diagnostic markers or therapeutic targets. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, barcreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in a patient for treating these
                                                                                                                                                                                                 Matches
                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                               Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New genes that are up-regulated or down-regulated in cancers, useful a markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
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20-SEP-2001; 2001US-0323887P.
13-NOV-2001; 2001US-0350666P.
08-FEB-2002; 2002US-0355145P.
08-FEB-2002; 2002US-0355257P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cancer related protein SEQ ID NO:303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Page 753; 767pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-SEP-2002; 2002WO-US029560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes an isolated nucleic acid molecule, which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heart
121
                              121
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                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
                                                                                                                                                                                                                 Similarity
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                 EVAISVTENIRQMDRSKRVTKNCIN
                                                               PSNGVPRSTAPGGI PNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK
                                                                                    SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR
                                                                                                                                                   MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP
                                                                                                                              MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
EVTINVIDSIQOMDRSRRITKNCVN
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2001US-0350666P.
2002US-0355145P.
2002US-0355257P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis; screening; modulator; leukaemia; ischaemia;
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                                                                                                                                                                                                             84.1%;
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Pred.
                                                                                                                                                                                                Mismatches
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No. 1
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..2e-62;
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RESULT 6
ADC31800
ID ADC31800
ID ADC3
XX ADC3
XX ADC3
XX ADC3
XX Huma
DE Huma
XX Huma

The invention relates to 971 novel human cDNA sequences (ADC29919-CC invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; and matibody against a polypeptide of the invention; and methods of cinvention further discloses methods of peventing, and methods of invention further discloses methods of peventing, and methods of ameliorating a medical condition; kits comprising polymclectide probes and/or monoclonal antibodies for carrying out the methods of the invention or activity of the jolymclectide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention (ADC31661-ADC32627) and the polypcptides encoded by the contigs (ADC332627) and the polypcptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the cidentification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are cidencer, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haley-Vicente
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; diagnostic; drug screening; forensics; gene mapping;
biodiversity assessment; Parkinson's disease; Alzheimer's disea
neurodegenerative diseases; anaemia; platelet disorder; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang
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Ghosh M,
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Ma Y, A
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Asundi V,
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Wang Z,
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Weng G;
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RESULT 7
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Best Local
The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful
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                                                                                                                                                                                                                                  Characterizing acute or chronic myelogenous leukemia, of in a patient comprises assaying for the overexpression BAALC transcripts in cells obtained from the patient.
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                                                                                                                                                                                  Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                     2003-441564/41.
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Pred. No. 1.2e-62;
                                                                                                                                                                                  English.
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        The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the chimeric construct; a vector comprising the nucleic acid fragment; obtaining a nucleic acid fragment encoding the polypeptide; a method for obtaining a polypeptide detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide, determining whether an agent alters the expression of PAIGB mRNA; screening separts for effectiveness in alters the expression of the nucleic acid fragment.
                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                   New nucleic acid fragment encoding a PAIGB polypeptide, useful preparing a composition for diagnosing, treating or preventing related disorders, e.g., osteoporosis.
                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for detecting BAALC overexpression. This sequence corresponds (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an spliced RNA consisting of exons 1, 6 and 8.
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animal; or
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RESULT 9
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Pred. No. 1.2e-62;
                                                                                                                                                                                                                                                                                                                                                   prostate cancer; Brain and Acute Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 145,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 121;
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                    WPI; 2003-441564/41.
N-PSDB; ADM46955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acute myelogenous leukemia; gene expression; BAALC; chronic myelogenous leukemia; prostate cancer; Brai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BALLC overexpression. This sequence corresponds to a BALLC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AN overexpression indicates that the patient has an aggressive form of AN overexpression indicates that the patient has an aggressive form of AN overexpression indicates that the patient has an aggressive form of AN overexpression indicates that the patient has an aggressive form of AN overexpression indicates that the patient has an aggressive form of AN overexpression indicates that the patient has an aggressive form of AN overexpression indicates that the patient has an aggressive form of AN overexpression indicates that the patient has an aggressive form of AN overexpression indicates that the patient has an aggressive form of AN overexpression indicates that the patient has an aggressive form of AN overexpression indicates that the patient has an aggressive form of AN overexpression indicates that the patient has an aggressive form of AN overexpression indicates that the patient has an aggressive form of AN overexpression indicates that the patient has an aggressive form of AN overexpression indicates that the patient has an aggressive form of AN overexpression indicates that the patient has an aggressive form of AN overexpression indicates the patient has a 
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                                                                                                        Tanner SM,
                                                                                                                                                                                                                   09-NOV-2001; 2001US-0348210P
                                                                                                                                                                                                                                                                                                                                 15-MAY-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic; exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brain and Acute Leukemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM46963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADM46963 standard; protein; 149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 19; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADM46953.
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                                                                                                     De La Chapell A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "encoded by GCS"
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67.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic alternate protein
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                                                         Claim 1; SEQ ID NO 2;
                                                                                                                                      polypeptide, useful for tumors, inflammations,
                                                                                                                                                                                                New polypeptide human
                                                                                                                                                                                                                                                                                                                                                                                                                                              29-SEP-2000; 2000CN-00125495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-SEP-2000; 2000CN-00125495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human dioxygenase 10.12
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                                                                                                                                                                                                                                                                                2002-509506/55
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                                                                                                                                                                                                                                                                                                                                                                                          SHANGHAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QCPNSQSLSSGPLTQKQNGLWTTE 109
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                                                                                                                                 ide human dioxygenase 10.12 and polynucleotides encoding useful for treating various diseases, such as malignant ammations, immunological diseases, hemopathy and HIV
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Pred. No. 1e-43;
2; Mismatches
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RESULT 12
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The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the chimeric construct; a vector comprising the nucleic acid fragment; obtaining a nucleic acid fragment encoding the polypeptide; a method for obtaining a polypeptide; detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody; an agent that alters the expression of PAIGB gene or polypeptide; determining whether an agent alters the expression of PAIGB mRNA; screening agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related
                                                                                                                                                                                                                                                                                   New nucleic acid fragment encoding a PAIGB polypeptide, useful preparing a composition for diagnosing, treating or preventing related disorders, e.g., osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dioxygenase 10.12, polynucleotides encoding this polypeptide, a DNA recombination process to produce the polypeptide and antagonist against the polypeptide. The present invention also discloses the method of applying the polypeptide in treating various diseases, such as malignant tumours, inflammations, immunological diseases, haemopathy and HIV infection. The present sequence is the human dioxygenase 10.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 92
                                                                                                                                                                                                                                                  Claim 9; SEQ ID NO 10; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-420299/39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       responsive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      animal; osteopathic; gene therapy; osteoporosis; mouse;
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72.78;
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Pred. No. 8.8e-29;
9; Mismatches 10
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bone
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RESULT 13
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Best Local
                                               Characterizing acute or chronic myelogenous leukemia, in a patient comprises assaying for the overexpression BAALC transcripts in cells obtained from the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                   09-NOV-2001; 2001US-0348210P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-NOV-2002; 2002WO-US036375
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                                                                                                                                                                                                                       2003-441564/41.
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Disclosure; SEQ ID NO 20; 78pp;

English

The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BRALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative

RNA consisting

of exons

6 and 8.

to a BAALC alternative

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RESULT 14
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Best Local
                                                                                                                                                                   Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                                                                                                           Disclosure; SEQ ID NO 18; 78pp; English.
                                                                                                                                                                                                                            N-PSDB; ADM46952.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one more BAALC transcripts in cells obtained from the patient, where an
                                                                                                                                                                                                                                                                                                                    09-NOV-2001; 2001US-0348210P
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chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acute Leukemia,
                                                                                                                                                                                                                                                                 De La Chapell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.5%;
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Pred. No. 1.1e-23;
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Query Match

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RESULT 15
ADO48477
The invention relates to a novel PTH responsive gene (PAIGB) fragment CC construct comprising the isolated nucleic acid fragment operatively CC linked to suitable regulatory sequences; a host cell transformed with the CC chimeric construct; a vector comprising the nucleic acid fragment; CC obtaining a nucleic acid fragment encoding the polypeptide; a method for CC ragment; an antibody that specifically binds to one or more epitopes of R PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody; an agent that alters the expression of PAIGB gene or polypeptide; a composition of PAIGB gene or polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide; a composition of PAIGB gene or polypeptide; a creening for agent alters the expression of PAIGB mRNA; CC screening squates for effectiveness in altering expression of the nucleic disorders; evaluating the efficacy of a treatment of a bone related CC disorders; evaluating the efficacy of a treatment of a bone related CC disorder in a subject; identifying polypeptides capable of binding to pAIGB; monitoring the effectiveness of treatment of a subject with a bone related agent; a transgenic animal comprising a first group of control animals; studying bone mass determinants; studying the modulation of bone mass; studying bone mass determinants; studying the modulation of bone for treating bone related disorders; identifying whether an agent which the related disorders; identifying whether an agent which has bone forming activity; and a stably transfected cell line comprising ctwo constructs, the first construct comprising a ligand binding domain which is linked to an activation domain
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ត្តនិត្តនិត្តនិត្តនិង្ស 문 S Query Match Best Local (Matches preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis. This sequence represents a PTH responsive gene protein of the invention. all of which expression is driven by a constitutive promoter, the second construct comprising multiple copies of DNA binding elements linked to a minimal promoter which is linked to PAIGB CDNA, where upon the addition of chemical inducer, transcription of PAIGB gene is induced. The PAIGB polynucleotide has osteopathic activity. The PTH responsive gene may be used to treat disorders by gene therapy. The nucleic acid is useful in Sequence 54 AA; 51; Similarity Conservative 36.2%; 1: Score 278; DB 8; Pred. No. 9.2e-23; Mismatches Length 54 Indels 0, 54 Gaps 54 0

Search completed: April 12, 2005, 15:37:16 Job time : 109.667 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-121-964-1
US-09-121-964-1
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Sequence 8115, Ap
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Sequence 2, Appli
Sequence 2, Appli
Sequence 10, Appli
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Sequence 473, App
Sequence 469, App
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RESULT 1 US-09-949-0 Sequence Patent NG GENERAL TITLE OF		22 22 24 24 24 24 24 24 24 24 24 24 24 2
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0-016-7117 Application US/0994901 NO. 6812339 INFORMATION: OF INVENTION: POLYMORPHISMS IN OF INVENTION: WITH HUMAN DISE EFFERENCE: CL001307 TT APPLICATION NUMBER: US/09/94 TT FILING DATE: 2000-04-14 APPLICATION NUMBER: 60/241, 755 FILING DATE: 2000-10-20 APPLICATION NUMBER: 60/237, 768 FILING DATE: 2000-10-03 FILING DATE: 2000-09-08 FILING DATE: 2000-09-08 TO SEQ ID NOS: 207012	^s/.	, , , , , , , , , , , , , , , , , , ,
J. Craig et al POLYMORPHISMS WITH HUMAN D. 101307 INWMBER: US/00-04-14 IUMBER: 60/241 IUMBER: 60/241 IUMBER: 60/337 IUMBER: 60/337 IUMBER: 60/331 IUMBER: 60		743 743 1002 1002 1002 1002 1002 1005 1095 1095 1095 174 244 715 177 177 177 177 178
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ON AND		Sequence
USES THEREOF		494, App 494, App 475, App 475, App 475, App 475, App 475, App 493, App 493, App 493, App 18465, A 117765, A

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RESULT 2
5198347-4
;PATENT NO. 5198347
;PATENT NO. 5198347
; APPLICANT: Miller, LOUIS H.;ADAMS, JOHI
; DAVIC C.;FANG, XIANGDOUG
; TITLE OF INVENTION: DNA ENCODING PLASM
;PLASMODIUM KNOWLESI DUFFY RECEPTOR
; NUMBER OF SEQUENCES: 27
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SOFTWARE: FastSEQ for Windows Version
; SEQ ID NO 7117
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7117
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Best Local (
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NO:4:
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Similarity 31.9%;
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Pred. No. 0.1;
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; DAVIC C.; FANG, XIANGOUG
TITLE OF INVENTION: DNA ENCODING PLASMODIUM VIVAX AND
; PLASMODIUM KNOWLESI DUFFY RECEPTOR
; PLASMODIUM KNOWLESI DUFFY RECEPTOR
; NUMBER OF SEQUENCES: 27
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION NUMBER: US/08/554,837
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8115
LENGTH: 726
                                                                                                                                                 Query Match
Best Local Similarity
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Patent No. 6562958
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
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                                                                                               GCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSA--AATDSG-----PEAGGLHAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDRSQGSLGPHIDERATLGETHMEKDIE 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVSSDVPSVGGKDSGPSTSASHALAGENGEVHNGTDTEPKEDGEKADPQKDIEVKGKQDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVSSDVPSVGGKDSGPSTSASHALAGENGEVHNGTDTEPKEDGEKADPQKDIEVKGKQDT
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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 -GPQASGDPRSAAP 244
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                                                                                                                                                 11.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Mismatches
                                                                                                                               8
                                                                                                                                                 Score 84; D:
Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 92.5; DB Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 92.5; DB Pred. No. 0.12;
                                                                                                                                 Mismatches
                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6;
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                                                                                                                               22;
                                                                                                                                                              Length 726
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                                                                                                                               Indels
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                                                                                                                               20;
                                                                                                                               Gaps
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                                                                 231
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Sequence 2, Application US/09408647A

Patent No. 639858

GENERAL INFORMATION:
APPLICANT: Kobayashi, Donald
IITLE OF INVENTION: Chitinase Gene from Stenotrophomonas
IITLE OF INVENTION: maltophila
IITLE OF INVENTION: maltophila
IITLE OF INVENTION: maltophila
IITLE OF INVENTION: MICHOPHILA
IITLE OF INVENTION: MICHOPHILA
IITLE OF INVENTION: MICHOPHILA
IITLE OF INVENTION NUMBER: US/09/408,647A
ICURRENT FILING DATE: 1999-08-26
PRIOR APPLICATION NUMBER: 60/098,036
PRIOR APPLICATION NUMBER: 60/098,036
PRIOR FILING DATE: 1998-08-27

NUMBER OF SEQ ID NOS: 2
SCPIWARE: FastSEQ for Windows Version 4.0
ISEQ ID NO 2
LENGTH: 700
ITYPE: PRT
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US-09-071-035-176
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US-09-408-647A-2
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 176, Application US/09071035
Patent No. 6448043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
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LOCATION: (1)...(41)
NAME/KEY: DOMAIN
LOCATION: (196)...(290)
NAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (330)...(483)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank No.
DATABASE ENTRY DATE: 1997-09-23
                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Stenotrophomonas FEATURE:
                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gil H. CH
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                      CITY: Rockville
                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 AQSGSISVT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 LVWSAATDNSGGSGVAGYDVYRNGSLVGSPSATQYTDGGLTASTAYTYTVRARDNAGNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 TWANASAGSHTFKAVATONNNAVTSSATVSVTVTASSNOTTPPSVPGGLASPSKTATTVN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 -----NCG-----TQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 TWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGPSSNGVLRPAAPGGIANPEKKM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                                                                                                                                           Maryland
Y: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AREVAISVT 127
                                                                                                                                                                                                                                                                          E: Human Genome Sciences,
9410 Key West Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.9%;
                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis Polynucleotides and Polypeptides
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Pred. No. 1.1;
14; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:

CLASSIFICATION:

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US-09-071-035-174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 174, Application US/09071035
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Best Local :
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                     ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.50
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Ver
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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Local Similarity 26.6%;
hes 47; Conservative 1
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STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 LTAATTSQADQNNFRVLYYAEKEAIPVNDARVNQLTPISSFEKKTYGSDAEAKNAVN 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 WTTEAKRDAKRMSAREVAISVTENIROMD-RSKRVT-------KNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 GLHAGVLEDGPSSNGVLRPAAPGGIANPEKKMN-CGTQCPN---SQSLSSGPLTQKQNGL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CGG-----SRADAIEPRYYESW----TRETESTWLTYTDSDALPSAAAT-DSGPEAG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STKEA-----ANNGSAEKQSPAKNANPDDQANQVLNQLANMFPGQGLPQAILTSQTNNF 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGGKSTENTDSRSSAAESTTVESTKASATKESSSK-ATTKSSDAKPSGTTTADSKATAS
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9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                         3.50 inch, 1.4Mb storage
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                                                                                                    PB369P2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 286;
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3 CGGSRADAIEPRY--YESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP

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; MOLECULE TYPE:
US-09-071-035-174
                                                                  ; MOLECULE TYPE: protein US-08-374-077C-2
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Best Loc
Matches
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Best Local Similarity
              Query Match
Best Local Similarity
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                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,077C
                                                                                                                                                                                                                                                                                    FILING DATE: 19-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zheng, Wei
APPLICANT: Dubald, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an Invertebrate Alphal
TITLE OF INVENTION: Calcium Channel Subunit
                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                   TELEPHONE: 703-836-2021
                                                                                                                                                                                                                                    NAME: McGowan, Malcolm M.
REGISTRATION NUMBER: 39,3
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22314-3187
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                                                                                                    TOPOLOGY:
                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 WTTEAKRDAKRMSAREVAISVTENIROMD-RSKRVT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 STKEA-----ANNGSAEKQSPAKNANPDDQANQVLNQLANMFPGQGLPQAILTSQTNNF 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 GLHAGVLEDGPSSNGVLRPAAPGGIANPEKKMN-CGTQCPN----SQSLSSGPLTQKQNGL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 CGGGKSTENTDSRSSAAESTTVESTKASATKESSSK-ATTKSSDAKPSGTTTADSKATAS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alexandria
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Ren, Dejian
Theng, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305
                                                                                                                                   2516 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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 Conservative
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10.2%; Score 78.5; I
22.4%; Pred. No. 27;
Live 21; Mismatches
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Pred. No. 0.98;
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                                 DB 3;
61;
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                               Length 2516;
 Indels 53;
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US-08-895-590-2
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Hall,
                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MCGOWAIN, MAICOIM M.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 022
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/00
FILING DATE: 19-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22314-3187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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APPLICANT: Dubald, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
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   308
                                                                  250 DDNSSY--SAVGGDSSSSNSCNCDITGDNSTLHGLGVGDVCSFIADCDDNSEDDDGDPNN
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GY: linear
                             QSLSSGPL-TQKQNGLWTTEAKRDAKRMSAREVAISVTENIRQMDRSKRVTKNC 143
                                                                                                                                                                   CGGSRADAIEPRY--YESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP 60
QDLSSQTLRTAAIVAAVAAAKEQAQEQSLADCE-SFSDRRQDADEDVRIIQDC
                                                                                                                                 CGGGGISAPPPRLTPEEAWQLQPQ------NSVTSAGSTNSSFSSGG-----GR 249
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                                                                                                                                                                                                      Conservative
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Pred. No. 27;
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RESULT 11
US-09-121-964-1
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Sequence 1, Application US/09121964
Patent No. 6124447
GENERAL INFORMATION:
APPLICANT: Natori, Shunji
TITLE OF INVENTION: NOVEL ENZYME CATALYZING DEPHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09539879A Patent No. 6436627 GENERAL INFORMATION:
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FILING DATE: 31-MAr-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/111,865
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/374,077
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 703-836-6620
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title OF INVENTION: Genes Encoding an Invertebrate Alphal
Calcium Channel Subunit
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LENGTH: 2516 amino acids
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Ren, Dejian
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                                                                                                                                                                       QDLSSQTLRTAAIVAAVAAAKEQAQEQSLADCE-SFSDRRQDADEDVRIIQDC 360
                                                                                                                                                                                                         QSLSSGPL-TOKONGLWTTEAKRDAKRMSAREVAISVTENIROMDRSKRVTKNC 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                Score 78.5; DI
Pred. No. 27;
Pred. Mismatches
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No
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; Sequence 104, Application US/09220528A
; Patent No. 6284540
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
APPLICANT: Milbrandt, Jeffrey D.
APPLICANT: Baloh, Robert H.
; TITLE OP INVENTION: Artemin, A No. 6284540el Neurotrophic Factor
FILE REFERENCE: 6029-7998
; CURRENT APPLICATION NUMBER: US/09/220,528A
; CURRENT FILING DATE: 1998-12-24
EARLIER FILING DATE: 1998-12-25
EARLIER FILING DATE: 1998-11-26
EARLIER FILING DATE: 1998-11-
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US-09-220-528-104
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; ORGANISM: Mus musculus
US-09-914-259-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FRANCSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 885
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Best Local 9
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APPLICANT: Makowski, Lee
APPLICANT: Hyman, Paul
APPLICANT: Williams, Ma
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LENGTH: 724
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APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
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CURRENT APPLICATION NUMBER: US/09/121,964
CURRENT FILING DATE: 1998-07-24
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SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGLHAGVLEDGPSSNGVLRPAAPGGI-----ANPEKKMNCGTQCPNSQSLSSGP---L 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSPRYPGRIFIPEYEHGHMTSTITPNNTNLGTQATNHASPQSG---KNGNGL 110
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28.6%;
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Pred. No. 5.1;
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US-09-620-405B-473
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Sequence 473, Application US/09433826B Patent No. 6579973 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
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APPLICANT: Jiang, Yuqiu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 495
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 473
LENGTH: 445
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NUMBER OF SEQ ID NOS: 120
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 104
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/620,405B CURRENT FILING DATE: 2000-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIACHOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 215
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                       194
                                                                                                                                                                                                                 134 DNDGFLKAPCRMKVSIPTKALELMDMQTFKAEPPEKPSAFEPAIEMQKSVPNKALELKNE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 AYWAPGPCD----RPRAPGPSASP---
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                                                                                                                                                                                                                                                   61 SSNGVLRPAAPGGIANPEKKM-----
                                                                                                                                                                                                                                                                                            78 RADEILPSESKQKDYEESSWDSESLCETVSQKDVCLPKAAHQKEIDKIN----GKLEESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 GVLEDGPSSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEA 110
                                                                                                                                                                                                                                                                                                                                7 RADAIEP----RYYESWTRETESTWLTYTDSD-ALPSAAATDSGPEAGGLHAGVLEDGP
                                                                                                                                                                                                                                                                                                                                                                      Similarity
37; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                       QTLRADQMFPSESKQKKVEENSWDSESLRET--VSQKDVCVPKATHQKEMDK 243
                                                                                                                                                                         QSLSSG---PLTQKQNGL----WTTEAKRDAKRMSAREVAISVTENIRQMDR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GARAAALGQRGRGAAACARSWCRCARSAWATAPTSWCVSASAAAPAAARA--LHTTSAWP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09620405B
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APPLICANT:
APPLICANT:

APPLICANT:

Jiang, Yuqui Dillon, Davin C. Mitcham, Jennifer L. Xu, Jiangchun Harlocker, Susan L.

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                       645
645
617.5
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1: /cgn2=6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2=6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

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16: /cgn2=6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

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Match Length
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    GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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US-10-293-239-20
US-10-293-239-20
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US-10-437-701-48905
US-10-425-114-65268
US-10-437-963-137075
US-10-282-122A-45268
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                Sequence 17, Appl
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Sequence 21, Appl
Sequence 20, Appl
Sequence 18, Appl
Sequence 22, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 48905, A
Sequence 65588, A
Sequence 65588, A
Sequence 137075,
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45	44	43	42	41	40	39	38	37	36	<u>ω</u>	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14
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445	215	1479	885	885	832	661	455	355	262	1013	1013	1013	661	661	661	305	305	305	286	286	286	508	320	670	600	1597	1491	609	539	1433	1433
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9-825-30	-09-220-920-1	10-437	10-37	-10-080	-10-087	5	-10-424-599-1936	4-599-	US-10-437-963-135251	-10-124-805-	-10-076-622-	-10-007-805-	-10-124-805-	-10-076-622-	10-007-805-	10-912-362-	76-	5-1	10-912-362-17	7	9-071-03	-10-437-963	10-425-114	-10-156-761	0-408-7	-10-437-963-18022	-10-437-963	-10-437-963-14498	-10-424-599	S-10-149-310	US-09-801-368-60
	í	1	Sequence 99, Appl	10, /	Φ	554,		æ	135	e 553,	e 553,	553	Sequence 552, App	552	552	e 174,	•	174,	176	æ	176,	e 188	e 43318,	æ	e 1945,	ര	m.	equence	e 22739	င္က	Sequence 60, Appl

ALIGNMENTS

US-10-293-239-17

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; ORGANISM: Homo sapiens
US-10-293-239-17
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Publication No. US20030119043A1
GENERAL INFORMATION:
APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR PILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
                                                                                                                                                                                                                                                           Query Match 84.1
Best Local Similarity 83.4
Matches 121; Conservative
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121 EVAISVTENIRQMDRSKRVTKNCIN 145
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121 EVTINVTDSIQQMDRSRRITKNCVN 145
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                                                                                                                                 61 SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTBAKRDAKRMSAR 120
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                                                                                       PSNGVPRSTAPGGI PNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK
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                                                                                                                                                                                                                                                                                    84.18;
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Publication No. US20030143743A1
GENERAL INFORMATION:
APPLICANT: Schuler, Gerold
APPLICANT: Schuler, Gerold
APPLICANT: N. V. Antwerps Innovatiecentrum
TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
TITLE OF INVENTION: Polynucleotides by Electroporation
FILE REFERENCE: 021505w0/JH/ml
CURRENT APPLICATION NUMBER: US(10/177,390
CURRENT PILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 34
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Best Local S
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Best Local
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SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
COURTENT FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
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TYPE: PRT
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                                                                                                                                                                                                                        y Match 80.5%; Score 617.5; DB 14; Local Similarity 67.2%; Pred. No. 5.5e-54; hes 121; Conservative 10; Mismatches 14;
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les 121; Conserv
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                                          61 KIKAPTDSVSDEGLFSASKMAPLAVFSHGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET
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                                                                                                                                                         1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHA------
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QCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAREVAISVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSVLEAEKS
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                                                                                       -GVLEDGPSSNGVLRPAAPGGIANPEKKMNCGT
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                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 73
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Best Local
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APPLICANT: de la Chapelle, Albert

TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia

FILE REFERENCE: 22727/04101

CURRENT APPLICATION NUMBER: US/10/293,239

CURRENT FILING DATE: 2002-11-12

PRIOR APPLICATION NUMBER: US 60/348,210

PRIOR PILING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 39

NUMBER OF SEQ ID NOS: 39
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APPLICANT: de la Chapelle, Albert
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 149
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                 Local Similarity
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                         MGCGGSRADAIBPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLED 58
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MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGCLEE 58
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                                                                                                 37.5%;
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                                                                              Score 288; DB 14;
Pred. No. 2.6e-21;
2; Mismatches 3;
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RESULT 6

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US-10-293-239-18
                                                                                                                                                                                                                        Sequence 37, Applica Publication No. US20 GENERAL INFORMATION:
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SEQ ID NO 22
LENGTH: 80
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Best Local Similarity
Matches 50; Conserv
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SEQ ID NO 18
LENGTH: 54
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Best Local Similarity 94.4%;
Matches 51; Conservative
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APPLICANT: Tanner, Stephan

APPLICANT: de la Chapelle, Albert

TITLE OP INVENTION: BAALC expression as a diagnostic marker for acute leukemia

FILE REFERENCE: 22727/04101

CURRENT APPLICATION NUMBER: US/10/293,239

CURRENT FILING DATE: 2002-11-12

PRIOR APPLICATION NUMBER: US 60/348,210

PRIOR APPLICATION DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 39
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APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
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APPLICANT: de la Chapelle, Albert
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
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No. US20030119043A1
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nilarity 94.3%;
Conservative
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Pred. No. 1.8e-20;
1; Mismatches 2;
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; FEATURE: ; OTHER INFORMATION: Clone ID: LIB3476-020-P1-K1-A12.pep US-10-767-701-48905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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; ORGANISM: Homo sapiens
US-10-293-239-37
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                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-767-701-48905
                                                                                                                                                         TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(5353)B CURRENT APPLICATION NUMBER: US/10/767,701 CURRENT FILING DATE: 2004-01-29 NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 48905
LENGTH: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 35
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                               Sequence 48905, Application US/10767701 Publication No. US20040172684A1 GENERAL INFORMATION:
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 Matches
                 Query Match
Best Local Similarity
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Best Local Similarity
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APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
                                                                                                                                                                                                                                                                                                          APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                        ORGANISM: Sorghum bicolor
                                                                                                                                           TYPE: PRT
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Conservative
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                 12.3%; Score 94; I
27.5%; Pred. No. 0
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17;
 Mismatches
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                                  DB 16; Length 147;
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 52;
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Indels 10;
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RESULT 12
US-10-437-963-137075
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US-10-425-114-65588
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                                                                                                                                                             NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 137075
LENGTH: 450
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APPLICANT:
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Best Local :
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LENGTH: 274
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                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5321)B CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5331)B
CURRENT FILLING DATE: 2003-04-28
CURRENT FILLING DATE: 2003-04-28
CURRENT FILLING DATE: 2003-04-28
CURRENT FILLING DATE: 2003-04-28
CONTRIBUTION SEES OF TABLES OF TA
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APPLICANT: Kovalic, David
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OTHER INFORMATION: Clone ID: PAT_MRT4530_38593C.1.pep
                                            TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wu, Wei
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Barbazuk, Brad
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Pred. No. 3.
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US-10-282-122A-45268
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PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
                                                                                                                                                                                                          SOFTWARE: PatentIn version
SEQ ID NO 45268
LENGTH: 718
                                                                  Matches
                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 45268, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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APPLICANT:
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                                                                                                                                                                                                                                                                      Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential FILE REFERENCE: ELITRA, 034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                   ORGANISM: Acinetobacter baumannii
                                                                                      Local
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2 GCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSA--AATDSG----PEAGGLHAG 54
                                                                ch 11.0%;
l Similarity 35.1%;
27; Conservative
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Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trawick, John
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Pred. No. 16;
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                                                                                                                                                                                                                                                                                             See File Wrapper or PALM
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                                                                                                       Length 718;
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173

GFGAGREDVWEPDNDVNWGDEKE--WLAHRNSEALAGSNLAATEMGLIYVNPE-----

223

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APPLICANT: Holtzman, Douglas
APPLICANT: Madden, Kevin T.
APPLICANT: Maxon, Mary
APPLICANT: Maxon, Mary
APPLICANT: Sherman, Amir
TITLE OF INVENTION: Modulation of Secondary Metabolite Production by
FILE REFERENCE: 14184-019US1
FILE OF INVENTION NUMBER: US/10/149,310
CURRENT APPLICATION NUMBER: US/10/149,310
CURRENT FILING DATE: 2003-02-19
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: WS 60/233,564
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-19
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                                                                                                                                                                                                                                                                                                                     Sequence 112, Application US/10149310 Publication No. US20040077039A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.8%; Score 83; DB 9; Length 1433; Best Local Similarity 29.4%; Pred. No. 49; Matches 32; Conservative 15; Mismatches 50; Indels
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SEQ ID NO 60
LENGTH: 1433
TYPE: PRT
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Patent No. Uszu-
Patent INFORMATION:
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APPLICANT: Sherman, Amir
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Silva, Jeff
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
FILE REPERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 06/160,587
PRIOR PILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Busby, APPLICANT: Cali,
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TUMBER OF SEQ ID NOS:
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Maxon, Mary
Milne, Todd
No. US20020128250Alman, Thea
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Holtzman, Doug
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Search completed: April 12, 2005, 16:03:42 Job time: 79.6667 secs
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Best Local 9
                                                                 980 GHSPMTNTTNGNKRLKYEKDAKR-NAKDGGISKGENAHNFQNDTKKNMS 1027
                                                                                                                                 927 LPPATTTSLKPLFGSQSKNSLENRQRTPNVKR-----ENPEHEYLYGNDSNNNNNSEA
                                                                                                  96 G--PLTQKQNGLWTTEAKRDAKRMSAREVAISVTENIR--QMDRSKRVT 140
                                                                                                                                                                   36 LPSAAATDSGPEAGGLHAGVLEDGPSSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSS 95
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Pred. No. 49;
15; Mismatches
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Minimum
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Perfect score:
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ALI GNMENTS	AB3048	T50113	T18222	JC5757	T31565	T13564	T08618	AF0611	JE0301	T35053	AG1028	I51172	C75521	T37193	T41551	AE2955
rs	8-amino-7-oxononan	3-dehydroquinate s	DNA polymerase del	DNA-directed DNA p	hypothetical prote	microtubule-associ	intrinsic factor-B	cell division prot	inulinase (EC 3.2.	. probable solute-bi	prepilin [imported	transcription fact	cytochrome-related	enamelin matrix pr	hypothetical prote	glutamyl-tRNA amid

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erythrocyte-binding protein - Plasmodium knowlesi
C;Species: Plasmodium knowlesi
C;Species: Plasmodium knowlesi
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 09-Jul-2004
C;Accession: A35970
R;Adams, J.H.; Hudson, D.E.; Torii, M.; Ward, G.E.; Wellems, T.E.; Aikawa, M.; Miller,
Cell 63, 141-153, 1990
A;Title: The duffy receptor family of plasmodium knowlesi is located within the microne
A;Reference number: A35970; MUID:91004213; PMID:2170017
A;Accession: A35970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: adult testis; clone DKFZp434L061 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein DKFZp434L061.1 - human C;Species: Homo sapiens (man) C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_(;Accession: T43456 R;Poustka, A.; Klein, M.; Mewee, H.W.; Gassenhuber, J.; W. submitted to the Protein Sequence Database, December 1999 A;Reference number: Z22516 A;Accession: T43456
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T43456
                                                                                                                                                                                                                                                                                                                                                                              RESULT
A35970
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A;Residues: 1-571 <AAA>
A;Cross-references: UNIPROT:075175; EMBL:AL133647
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C; Superfamily: hydroxyproline-rich glycoprotein
                                                                                  A;Cross-references: UNIPROT:P22545; GB:M68518; GB:M37513; NID:g160273; C;Keywords: transmembrane protein
                                                                                                                          A; Molecule type: DNA
A; Residues: 1-778 < ADA>
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Query Match
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Matches 29; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 ALGPKASPAPSHNSGTPAPYAQAVAPPAPSGPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 -- GGIANPEKKMNCGTQCPNSQSLS----SGPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 TDSDALPSAAATDSGPEAGGLH-------AGVLEDGPSSNGVLRPAAP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDSEVSQSPAKNGSKPVHSNQHPQSPAVPPTYPSGPPPAASALSTTPGNNGVPAPAAPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann,
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.1%;
                   12.1%;
  12;
Score 92.5; DE Pred. No. 1.4; 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 92.5; DB Pred. No. 0.95;
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                                         DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
    44;
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                                         Length 778;
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  Indels
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                                                                                                      PID:g160274
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Ajbayera...
R;Grzesitza, D.
submitted to the EMBL Data Library,
submitted to the EMBL Data Library,
submitted to the EMBL Data Library,
R;Boles, E.; Hettmann, C.; Zimmermann, F.K. submitted to the EMBL Data Library, December 1995 A;Reference number: S61594
                                                                                                                                                                                                                                                                                                                                                           R;Pearson, D.; Bowman, S. submitted to the EMBL Data Library, May 1995 A;Reference number: S54582
                                                                 A; Molecule type: DNA
A; Residues: 1-746, 'L', 748-1433 <GRZ>
A; Cross-references: EMBL: X78344; NID: 9559523; PIDN: CAA55139.1; PID: 9559524
                                                                                                                                               A; Reference number: A; Accession: S48234
                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Saccharomyces cerevisiae C;Date: 08-Jul-1995 #sequence revisic C;Accession: S54587; S48234; S61595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Unexpected sequence diversity in the amino-terminal ends of the coat proteins A;Reference number: PHO207; MUID:91132116; PMID:1993866
A;Recession: PHO207
A;Molecule type: genomic RNA
A;Residues: 1-365 <FRE>
A;Cross-references: UNIPROT:PZ5242; GB:D00948; NID:g222123; PIDN:BAA00796.1; PID:g22212
C;Superfamily: tobacco etch virus genome polyprotein
C;Keywords: coat protein; inclusion protein
F;1-52/Product: nuclear inclusion protein b (fragment) #status predicted <IPB>
F;53-365/Product: coat protein #status predicted <COA>
                                                                                                                                                                                                                                                                   A;Residues: 1-1433 <PEA>
A;Cross-references: UNIPROT:P39113;
                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: S54587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Contains: carboxyl end of nuclear inclusion prote: C;Species: sugarcane mosaic virus, SCMV C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 : C;Accession: PH0207 R;Frenkel, M.J.; Jilka, J.M.; McKern, N.M.; Strike, J.Gen. Virol. 72, 237-242, 1991
                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N; Alternate names: MSP8 protein;
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N;Contains: carboxyl end of nuclear inclusion protein b; coat protein
C;Species: sugarcane mosaic virus, SCMV
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                              A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
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Best Local S
Matches 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AISVTENIROMDRSKRVTK 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIKEEEIE-KYFKQFAKDLPGYLEDYND-EVFHQAGTVDAGAQGGGGNAGTQPPATGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGVLRPAAPGGIANPEKKWNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAREV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDSDALPSAAATDSGPEAGGLHAGVLEDGPSSNGV-LRPAAPGGIANPEKKMNC-GTQCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGGAQPPATGAAAQPPTTQ--GSQLPQGGATGGGGAQTGAGGTGSVTGGQRDKDVDAGTT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVL--EDGPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVSSDVPSVGGKDSGPSTSASHALAGENGEVHNGTDTEPKEDGEKADPQKDIEVKGKQDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDRSQGSLGPHTDERATLGETHMEKDTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSOSLSS-GPLTQKQNGLWTTEAKRDAK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uclear inclusion protein b (fragment)
coat protein #status predicted <COA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.5%;
                                                                                                                                                                                                                                              AB972
                                                                                                                                                                                                                                                                                                                                                                                                                                      revision 01-Sep-1995 #text_change 16-Aug-2004
$61595; $49498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein YM8021.06c; protein YMR280c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.5,
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 88; DB Pred. No. 1.5;
                                                                                                                                                                                                                                                                     EMBL: Z49704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 365
                                                                                                                                                                                                                                                                     NID:g825540;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN:BAA00796.1; PID:g22212
                                                                                                                                                                                                                                                                     PIDN:CAA89778.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  411
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                                                                                                                                                                                                                                                                   PID: 98255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ס.ם.
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A; FULL CARIS A; Residues: 1-967 < ARIS A; Cross-references: UNIPROT: Q08294; A; Cross-references: Strain S288C

EMBL: Z74897; NID: g1420063;

PID:e251930; PID:g1420064

A; Reference number: \$66814 A; Accession: \$66852

A; Molecule type: DNA

R;Arino, J.; Casamayor, A.; Gamo, F.J.; Gano, submitted to the Protein Sequence Database,

C;Species: Saccharomyces cerevisiae C;Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text_change 09-Jul-2004 C;Accession: S66852; S66854; S67325; S70380

F.J.; Gancedo,

July

C.; 1996

Lafuente,

M.J.;

Aldea,

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Casas, റ hypothetical protein YOL155c - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein 00419; protein AOF1001

S66852 RESULT

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                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from A;Molecule type: DNA A;Residues: 1-269 <SAN A;Cross-references: UNIPROT:Q9S1Y3; EMB A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data A; Reference number: Z21621 A; Accession: T37073
                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: T37073
R;Sanders, D.C.; Harris, D.; Bentley, S.D.; Parkhill,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein SCJ30.06c - Streptomyces C;Species: Streptomyces coelicolor C;Date: 03-Dec1-999 #sequence_revision 03-Dec-C;Accession: T37073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 13R
C;Superfamily: GAL4 zinc binuclear cluster homology
C;Keywords: transmembrane protein
C;Keywords: transmembrane duster homology <0
F;65-102/Domain: GAL4 zinc binuclear cluster homology <0
F;456-472/Domain: transmembrane #status predicted <TM1>
F;738-754/Domain: transmembrane #status predicted <TM2>
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A;Croos-references: EMBL:X94215; NID:g1122900; PIDN:CAA63906.1; PID:e214033; PID:g112290
A;Experimental source: strain ENY.WA-1A
C;Genetics:
                                                                                                                                                                                                                                         A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references:
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                                                                                                                                                              Matches
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Best Local
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                                                                                                                                                                                                                                         SCOEDB:SCJ30.06c
                                       61
                                                                                                                    11 IEPRYYESWT------RETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP
                                                                                                                                                            26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 LPSAAATDSGPEAGGLHAGVLEDGPSSNGVLRPAAPGGIANPEXKMNCGTQCPNSQSLSS
-GGGVVTTGAGGGIV-PGEACRCGRAAHAPTNASMRS
                                     SSNGVLRPAAPGGIANPEKKMNCG--TQCPNSQSLSS
                                                                             LPPTHVEQWVPVNFHCRPRRRVLRSGGLTFSPTTVLPSRGCCGSGERTGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHSPMTNTTNGNKRLKYEKDAKR-NAKDGGISKGENAHNFQNDTKKOMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPPATTTSLKPLFGSQSKNSLENRQRTPNVKR-----ENPEHEYLYGNDSNNNNNSEA
                                                                                                                                                            Conservative
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                                                                                                                                                                             10.6%;
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                                                                                                                                                          9;
                                                                                                                                                          Score 81; DB:
Pred. No. 4.6;
9; Mismatches
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                                                                                                                                                                                                                                                                                                    EMBL:AL109973; PIDN:CAB53301.1; GSPDB:GN00070; SCOED
                                                                                                                                                                                                                                                                                                                                                                                                                      August
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                                                                                                                                                                               4.6;
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                                                                                                                                                                                                  2
                                                                                                                                                            38;
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                                       95
                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                             J.; Barrell,
                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <GAL4>
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                                                                                                                                                            Gaps
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probable guanine nucleotide exchange fa
N;Alternate names: Shar pei/DRhoGEF2
C;Species: Drosophila melanogaster
C;Date: 11-Jun-1999 #sequence_revision
C;Accession: T09144; T09223
R;Haecker, U.; Perrimon, N.
submitted to the EMBL Data Library, Oct
A;Reference number: Z16586
A;Accession: T09144
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A;Residues: 1-164, 'STSITSGSSSATESGSSVSGSTSATESGSSASGSS',166-186,'V',188-967
A;Residues: 1-164, 'STSITSGSSSATESGSSVSGSTSATESGSSASGSS',166-186,'V',188-967
A;Cross-references: EMBL:X89715; NID:g1177620; PID:e190152; PID:g1177622
R;Gamo, F.J.; Laftente, M.J.; Casamayor, A.; Arino, J.; Aldea, M.; Casas, C.
Yeast 12, 709-714, 1996
A;Title: Analysis of the DNA sequence of a 15,500 bp fragment near the left and two new open reading frames.
A;Reference number: S70379; MUID:96405919; PMID:8810044
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A;Experimental source: strain S288C
R;Gamo, F.J.; Laftwente, M.J.; Cassamayor, A.; Aldea, M.; Casas, C.; Ario, J.; Herrero, E submitted to the EMBL Data Library, July 1995
A;Description: Analysis of the DNA sequence of a 15500 bp fragment of the left arm of c
                                                                                                                                                                                                                                                                                                                         Cell 91, 905-915, 1997
A;Title: The Rho GTPase and a putative RhoGEF mediate a
A;Reference number: Z16618; MUID:98088790; PMID:9428514
A;Accession: T09223
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A; Reference number: 867324
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submitted to the
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;Residues: 1-2559 <HAE>
;Cross-references: UNIPROT:O44113; EMBL:AF031930; NID:g2687355;
;Cross-references: UNIPROT:O44113; EMBL:AF031930; NID:g2687355;
Map position: 2;
                                                                                                                                                            Residues: 1-676,'L',678-837,'L',839-889,'S',891-1243,'D',1245-1358,'E',1360-1368,'R',C',1265-1368,'R',C',1265-1368,'R',R',1360-1368,'R',R',1360-1368,'R',C',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1368,'R',1360-1
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;Residues: 1-676,'L'
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Cross-references: EMBL:X89715
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;Residues: 55-164,'8
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A;Note: orchestrates CHI BINGE CHITS STATES A;Note: orchestrates CHITS STATES A;Note: orchestrates CHITS C;Function: C;Function: mediates actin rearrangements required for cell shape changes during A;Description: mediates actin rearrangements required for cell shape changes during C;Superfamily: rat Munc13-3 protein; protein kinase C zinc-binding repeat homology <KZN>
                                                                                                                                                           A kinase anchor protein AKAP-KL isoform 1 - mouse (Species: Mus musculus (house mouse) (C;Date: 11-Jun-1999 #sequence revision 11-Jun-1999 #text (C;Accession: T09225; T09226; T09227 R;Dong, F:; Feldmesser, M.; Casadevall, A.; Rubin, C.S. J. Biol. Chem. 273, 6533-6541, 1998 A;Title: Molecular characterization of a cDNA that encod A;Reference number: Z16620; MUID:98165844; PMID:9497389 A;Accession: T09225
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C;Species: Rattus norvegicus (Norway rat)
C;Apate: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A40670
R;Hallberg, E; Wozniak, R.W.; Blobel, G.
J. Cell Biol. 122, 513-521, 1993
                                                                                                A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-885 < DON>
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A;Residues: 1-1199 <HAL>
A;Cross-references: UNIPROT:P52591; GB:Z21513; NID:g396746; PIDN:CAA79725.1;
A;Cross-references: UNIPROT:P52591; GB:Z21513; NID:g396746; PIDN:CAA79725.1;
F;803-807,845-849,956-960,1010-1014,1047-1051,1076-1080/Region: pentapeptide
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                                                        A;Cross-references: UNIPROT:O54931; EMBL:AF033274; NID:g2852696; A;Note: binds the regulatory subunits (RII) of protein kinase AII
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                                        A; Accession: T09226
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;Status: preliminary;
;Molecule type: mRNA
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PMID:8335683
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: The sequence of C. elegans cosmid F12F3.
A;Reference number: Z21521
A;Accession: T34418
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3488 <FUL-
A;Cross-references: EMBL:U80022; PIDN:AAC25885.1; GSPDB:GN00023; CESP:F12F3.
A;Experimental source: strain Bristol NZ; Clone F12F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-848,862-885 <DO2>
A;Cross-references: EMBL:AF033275; NID:g2852698; PID:g2852699
A;Oross-references: EMBL:AF033275; NID:g2852698; PID:g2852699
A;Note: binds the regulatory subunits (RII) of protein kinase AII isoforms
A;Accession: T09227
A;Accession: T09227; translated from GB/EMBL/DDBJ
A;Statue: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule: type: mENNA
A;Residues: 1-789,'PGGHTG' <DO3>
A;Cross-references: EMBL:AF033276; NID:g2852700; PID:g2852701
A;Note: binds the regulatory subunits (RII) of protein kinase AII isoforms
C;Genetics:
                                                                           C;Date: 05-Dec-1997
C;Accession: C69899
                                                                                                    C;Species: Bacillus
C;Date: 05-Dec-1997
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                                                                                                                                                  conserved hypothetical protein yobL
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A;Map position: 5
A;Introns: 281/3; 332/1;
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Best Local S
Matches 33
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Pred. No. 1.6e
23; Mismatches
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Pred. No. 34;
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holseappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                       A;Gene: FlyBase:5-HT1B
A;Cross-references: FlyBase:FBgn0004572
C;Superfamily: octopamine receptor type
C;Keywords: G protein-coupled receptor;
F;124-145/Domain: transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-645 <SAU>
A;Cross-references: UNIPROT:P28286; EMBL:Z11490; NID:g7506; PIDN:CAA77571.1; PID:g7507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBO J. 11, 7-17, 1992
A;Title: A family of Drosophila serotonin receptors with distinct
A:Reference number: S19155; MUID:92155185; PMID:1310937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N/Alternate names: 5-hydroxytryptamine C;Species: Drosophila melanogaster C;Date: 07-Apr-1994 #sequence_revision C;Accession: S19156; S18154
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A; Residues: 1-600 «KUN»
A; Cross-references: UNIPROT:034330;
A; Experimental source: strain 168
C; Genetics:
                                                                                                                                                                                                                                      F;234-256/Domain: transmembrane F;284-305/Domain: transmembrane
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A; Accession: S19156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    serotonin receptor 28 - fruit fly (Drosophila melanogaster) N;Alternate names: 5-hydroxytryptamine receptor 2B (5-HTR2B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S19156
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                                                                                                                                                                                                                 ;564-587/Domain:
                                                                                                                                                                                                                                                                                         ;193-214/Domain:
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                                                                                Conservative
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                                                                                                                                                                                                                 transmembrane
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                                                                                                        31.0%;
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23.1%; Pred. No. 30;
tive 23; Mismatches
                                                                                                                                9.9%;
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                                                                                                        Score 76; DE
Pred. No. 36;
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                                                                                Mismatches
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s predicted <TM1>
s predicted <TM2>
s predicted <TM3>
s predicted <TM3>
s predicted <TM4>
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s predicted <TM7>
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A;Molecule type: mRNA
A;Residues: 1-499 < DUII>
A;Residues: 1-499 < DUII>
A;Cross-references: UNIFROT:Q99MK3; EMBL:X60469; NID:g57559; PIDN:CAA42999.1; PID:g57560
A;Cross-references: UNIFROT:Q99MK3; EMBL:X60469; NID:g57559; PIDN:CAA42999.1; PID:g57560
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 31-318 < DUIZ>
A;Residues: 31-318 < DUIZ>
A;Cross-references: EMBL:X60468; NID:g57561; PIDN:CAA42998.1; PID:g1177617
A;Note: this sequence was submitted to the EMBL Data Library, July 1991
C;Genetics: 88/3; 107/3; 135/3; 157/3; 207/3; 250/2; 252/2; 290/3
C;Keywords: transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Spec
C;Date
C;Acce
R;Lin,
                                                                                                                                                                                                                                                                                                                                                                                                 R;Duilio, A.; Zambrano, N.; Mogavero, A.R.; Ammendola, R.; Cimino, F.; Russo, Nucleic Acids Res. 19, 5269-5274, 1991
A;Title: A rat brain mRNA encoding a transcriptional activator homologous to A;Reference number: $22571; MUID:92020215; PMID:1923810
A;Accession: $22571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 integrase-like protein FE65 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 02
C;Accession: $22571; $22572
R;Duilio, A; Zambrano, N.; Mogavero, A.R
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C; Genetics:
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A; Residues: 1-839 <STO>
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A; Accession: E84824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: E84824
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein At2g40040 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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  Query Match
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Best Local
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ch 9.8%;
l Similarity 25.6%;
34; Conservative 1
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       17;
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  Score 75.5; D
Pred. No. 30;
17; Mismatches
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Pred. No. 4
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49;
                                              DB 2;
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    59;
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                                            Length 499;
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R;Bahri, S.M.; Yang, X.Y.; Chia, W.

Mol. Cell. Biol. 17, 5521-5529, 1997

Mol. The Drosophila bifocal gene encodes a novel protein A;Reference number: Z15048; MUID:97415628; PMID:9271427

A;Accession: T03743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
T03743
T03743
bifocal protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #t
C;Accession: T03743
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                                133 MDRSKRVT 140
                                                                                                                                         143 NVTVTPIPKORSSLLNTRSQEREMVRYILSESGERDGELESGEOPAGVVSNSRCGEVETG
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                                                                                                      73 GIANPEKKMNCGTOCENSOSLSSGPLTOKONGLWTTEAKRDAKRMSAREVAISVTENIRO 132
                                                                                                                                                                                                                                                                                  39;
                                                                                                                                                                                                                                                 5 GSRADAIEPRYYESWTR------ETESTWLTYTDSDAL-------PSAAAT- 42
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STRAIN-C57BL/6J; TISSUE-Cerebellum;

MEDLINB-20530913, PubMed-11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

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Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUB=Cerebellum;
MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
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   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Ca
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hiroza
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasuka
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda
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STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
"Functional annotation of a full-length mouse cDNA colle
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25-OCT-2004 (TrEMBLrel. 28, Last and update)
BAALC isoform 1-6-8 (Mus musculus 16 days neonate cerebellum cDNA,
RIKEN full-length enriched library, clone:9630028H16 product:brain
acute leukemia, cytoplasmic, full insert sequence).
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[5]
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Nature 420:563-573(2002).
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                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE-Cerebellum; The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carninci P., Hayashizaki Y., "High-efficiency full-length cDNA cloning Meth. Enzymol. 303:19-44(1999).
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Hirozane T.,
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Kouda M., Koya (
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RC TISUE-Whole embryo;

RC PubMed=14702039; DOI=10.1038/ng1285;

RD Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

RA Wakamatsu A., Haysshi K., Sato H., Nagai K., Kimura K., Makita H.,

RA Wakamatsu A., Haysshi K., Sato H., Nagai K., Kimura K., Makita H.,

RA Wakamatsu A., Dayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nagahari K.,

RA Watakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,

RA Yamamoto J., Saito K., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

RA Sudo H., Hosoiri T., Kaku Y., Xodaira H., Kondo H., Sugawara M.,

RA Sudo H., Hosoiri T., Yamashita H., Kondo H., Sugawara M.,

RA Sudo H., Kamata K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,

RA Minomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,

RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,

RA Nono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,

RA Togiya S., Komat F., Hara R., Takeuchi K., Arita M., Imose N.,

RA Noriya S., Momiyama H., Satoh N., Takami S., Terashima Y.,

RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Wakebe H.,

RA Wasashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,

Yamazaki M., Watanabe K., Kumagai A., Itakura S., Bukuzumi Y.,

Yamazaki M., Watanabe K., Kumagai A., Itakura S., Pukuzumi Y.,

RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Pukuzumi Y.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Matagawa S., Sakama M., Tashiro H., Tanigami A., Sasaki M.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Moriya R., Sakami Y., Mizuno T., Morinaga M., Sasaki M.,

RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
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EMBL; AR079337; BAC37611.1; -.
Pfam; PPG6989; BAALC N; 1.
Pfam; PPG6989; BAALC N; 1.
SEQUENCE 145 AA; 15515 MW; 4972670A618C4D6D CRC64;
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01-MAR-2001
01-MAR-2001
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein FLJ12015 (BAALC isoform 1-6-8)
leukemia, cytoplasmic) (BAALC 1-6-8)
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eda Y., Tanaka T
Hayashizaki Y.;
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AK Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

AK Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

AK Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

AHOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

AN Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

AN Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

AN Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

AN Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

AN Hopkins R.F., Jordan R.J., Farmer A.A., Rubin G.M., Hong L.,

AN Stapleton M., Soares M.B., Boutow K.F., Casavant T.L., Scheetz T.E.,

AN Stapleton M., Godernan R.J., Malek J.A., Gunaratne P.H.,

AN Hitlan S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

AN Hitlan D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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MEDLINB-21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;

MEDLINB-21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinoner Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,

Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;

"BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia.";

Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Q8WXS3;
Q8WXS3;
Q1-MAR-2002 (Tx)
Q1-MAR-2004 (Tx)
Q1-MAR-2004 (Tx)
BAALC 1-5-6-8.
                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;

MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinoner Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;

"BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia.";

Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).

EMBL; AF363578; AAL50379.1; -.

Pfam; PF06999; BAALC N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498; Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinoner Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; "BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia."; Proc. Matl. Acad. Sci. U.S.A. 98:13901-13906(2001). EMBL; AF371322; AAL50518:1; -. Pfam; PF06989; BAALC_N; 1. 975ED7D00EF82E26 CRC64;
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01-MAR-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
BAALC isoform 1-6-8.
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Mammalia; Eutheria;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2810457D07 product:brain and acute leukemia,
cytoplasmic, full insert sequence.
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01-MAR-2002
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                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
           SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636;
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                                                                                                                Name=Baalc;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                               QCPNPQSLSSGPLTQKQNGLQTTE 144
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Hayashizaki
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AA; 15577 MW;
                                                                         Chordata;
Rodentia;
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Primates;
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Pred. No. 7.5e-
2; Mismatches
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                                                                         Craniata; Ver
Sciurognathi;
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                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB26C19969B91F6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                           473.5;
           DOI=10.1016/S0076-6879(99)03004-9;
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chi; Muridae; Murinae; Mus
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STRAIN-C57BL/6J; TISSUE-Whole body;

STRAIN-C57BL/6J; TISSUE-Whole body;

WHEDLINE-20530913; PubMed-11076861; DOI=10.1101/gr.152600;

XM Shibata K., Itch M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

XA Shibata K., Itch M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

XA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,

XA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

XA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

XA Yamamoto R., Matsumoto H., Togawa Y., Izawa M., Ohara B., Watahiki M.,

XA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

XA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

XA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Hayashizaki Y.;

XI "RIKEN integrated sequence analysis (RISA) system-384-format

Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                              CC STRAINCESTBLIGHT TISSUE=Whole body;

Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

A Kawai J., Kojima Y., Konno H., Saito H., Saito R., Sakai C., Sakai K.,

A Chazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

A Chazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

A Chazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

A Sogabe Y., Suzuki H., Tagami M., Tagami A., Takahashi F., Tanaka T.,

A Sogabe Y., Suzuki H., Tagami M., Tagami A., Yoshida K., Yoshino M.,

A Muramatsu M., Hayashizaki Y.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                      Best
                                                                                                                                                                               Matches
                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                        EMBL; AK013358; BAB28808.1; -. MGD; MGI:1928704; Baalc.
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the RIKEN Genome Exploration Research Group
"Analysis of the mouse transcriptome based o
60,770 full-length cDNAs.";
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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STANDARD TISSUE=Whole body;
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STRAIN=C57BL/6J; T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                    Local
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91
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                                                                                                                AGVLEDGÞSSNGVLRÞAAÞGGIANÞEKKMNCGTQCÞNSQSLSSGÞLTQKQNGLWTTEAKR
                                       DAKRMSAREVAISVTENIROMDRSKRVTKNCIN
                                                                                                                                                                                                                                                                        123 AA;
                                                                                                                                                                             59.8%;
larity 94.6%;
Conservative
                                                                                      SSNGVLRPAAPGGIANPEKKWNCGTQCPNSQNLSSGPLTQKQNGLWATEAKR
                                                                                                                                                                                                                                                                      13391 MW;
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                                                                                                                                                                             Score 459; DB Pred. No. 1.2e 3; Mismatches
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on functional annotation
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MEDLING-21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinoner Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,

Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;

"BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia.";

Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heine Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; "BAALC, the human member of a novel mammalian neuroectoderm guineage, is implicated in hematopoiesis and acute leukemia.", Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).

BMBL, AP371324; AAL50520.1; -. MGD; MGI:1928704; Baalc.
Pfam; PF06899; BAALC N; 1.

SEQUENCE 54 AA; 5667 MW; FEE8COEBFBCDB829 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
BAALC 180form 1-8.
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STRAIN-12986/SvEvTac;
MEDLINE-21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
MEDLINE-21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
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05-JUL-2004
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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BAALC isoform 1-8.
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01-MAR-2002
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MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG
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Pred. No. 3.3e-19;
0; Mismatches 0;
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Pred. No. 3.3e-19;
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                                                                                              Сарв
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RESULT
QAWXSO
ID
Q8
AC Q8
DT 011
DT 011
DT 011
DT 011
DT 011
DT 01
DT 01
RP BA
GN NA
GN NA
GN NA
TA
RA TA
RA MT
RA TA
RA
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Q8WTP6
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Best Local
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

DOI=10.1073/pnas.241525498;

MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen Mrozek K., Sill H., Knuutila S., KOlitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;

"BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia.";

Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).

EMBL; AF363578; AAL50380.1; -.

Pfam; PP06989; BAALC N; 1.

SEQUENCE 73 AA, 7871 MW; 98DBC2B6E6EF524A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8WTP6
Q8WTP6;
01-MAR-2002 (TrEMBI
01-MAR-2002 (TrEMBI
05-JUL-2004 (TrEMBI
BAALC isoform 1-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8WXS0;
Q8WXS0;
01-MAR-2002
01-MAR-2002
Strausberg R.I., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498; Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinoner Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; "BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopolesis and acute leukemia."; proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=BAALC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAALC 1-4-5-6-8.
                                                                                                                                                                                                                                                                                                                                     MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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(TrEMBLrel.
(TrEMBLrel.
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(TremBLrel. 20, Last sequence up
(TremBLrel. 27, Last annotation
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Primates;
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Primates;
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Pred.
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Last sequence update)
Last annotation updat
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No. 1
                                                                                                                                                                                                                                                                                                                                     DOI=10.1073/pnas.242603899;
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.6e-18;
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RESULT
QBWXS2
ID WXS2
ID QB
AC QB
DT 011
DT 011
DT 011
DT 011
DT 011
DT 011
RN BAH
GN NA
GN NA
GN NC
RN NC
RN (11
RP SHE
RA MIZ
RA MIZ
RA MIZ
RA MIZ
RA P1
RT 11
RT 11
RT P1
RT P1
RT P1
RT P1
 RESULT
Q8WNE8
ID Q8
AC Q8
DT 01
DT 01
DT 01
DT 01
DT 01
ON NA
GN NA
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Best Local S
Matches 50
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Submitted (JUL-2002) to the EMBL/
Submitted (JUL-2002) to the EMBL/
EMBL; AF371323; AAL50519.1; -.
EMBL; AF363578; AAL50378.1; -.
R Pfam; PF06989; BAALC N; 1.
R Pfam; PF06989; BAALC N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 51; Conserv
                      Q8WNE8 PRELIMI
Q8WNE8;
01-MAR-2002 (TrEMBL
01-MAR-2002 (TrEMBL
01-MAR-2004 (TrEMBL
BAALC isoform 1-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QBWXS2;
01-MAR-2002
01-MAR-2002
01-MAR-2004
                                                                                                                                                                                                                                                                                 "BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia."; Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
EMBL; AF365578; AAL50382.1; -.
Pfam; PF06989; BAALC_N; 1.
               Name=BAALC;
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498; Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heino Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones S.J., Marra M.A., "Generation and initial analysis and mouse cDNA sequences", proc. Natl. Acad. Sci. U.S.A. 99:
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                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=BAALC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8WXS2
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                      13
scrofa (Pig)
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                                                                                                                                                                                                                 50;
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                                                                                                                                                                             MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHA
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2 (TrEMBLrel.
4 (TrEMBLrel.
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nilarity 94.3%;
Conservative
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(TrEMBLrel.
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                                                                                             PRELIMINARY;
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AA; 8573 MW;
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Primates;
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94.4%;
                                        20,
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                                                                                                                                                                                                                ; Score 272; DB
; Pred. No. 5e-1
1; Mismatches
                                        Created)
Last sequence
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last seq
Last anno
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Pred. No. 9e-1
1; Mismatches
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                                       sequence update)
annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of more than 15,000 full-length
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No. 9e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
                                                                                                                                                                                                                              5e-17;
                                                                                                                                                                                                                                            DB 2;
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RESULT 15
Q6ZMJ6
ID Q6ZMJ
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Q6ZMJ6; O5-JUL-2004 (TrEMBLrel. 2:
05-JUL-2004 (TrEMBLrel. 2:
05-JUL-2004 (TrEMBLrel. 2:
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MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen Mrozek K., Sill H., Knuttila S., Kolitz J.B., Archer K.J.,

Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;

"BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia.";

Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).

EMBL; AF371326; AAL50522.1; -.

Pfam; PF06599; BAALC_N; 1.

SEQUENCE 54 AA; 5681 MW; 6538C3DABED9B825 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PFO
NON TER
SEQUENCE
Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI TaxID=9606; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinopterygii; Neopterygii; Cyprinidae; Danio. NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name-SI:ZC215113.3;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Chordata; Craniata; Vertebrata;
                                                                                           Homo sapiens (Human).
                                                                                                              FLJ00420 protein
Name=FLJ00420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2003) to the EMBL/GenBank/DDBJ EMBL; AL807244; CAD87801.1; -. Interpro; IPR09728; BAALC N.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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1 (Fragment).
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                                            Craniata; Vertebrata; Catarrhini; Hominidae;
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RP SEQUENCE FROM N.A.

RC TISSUE-Spleen;
RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
REBL, Ak160386; BAD18729.1; IEA.
DR EMBL, Ak160386; BAD18729.1; IEA.
DR GO; GO:003528; F:transcription regulator activity; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR010797; Not N.
DR InterPro; IPR010797; Not N.
DR InterPro; IPR010797; Not N.
DR Pf4m; PF04065; Not3; 1.
PT NON TER
SQ GO:003528; F:transcription regulator activity; IEA.
DR Pf4m; PF04065; Not3; 1.
PT NON TER
SQ SEQUENCE 613 AA; 64243 MW; 8D78E87BD58F9E2C CRC64;
SEQUENCE 613 AA; 64243 MW; 8D78E87BD58F9E2C CRC64;
SEQUENCE 613 AA; 64243 MW; 8D78E87BD58F9E2C CRC64;
SQ GO:00045449; P:regulator regulator regu
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

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US-09-949-016-8824
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US-09-949-016-11662
US-09-086-663A-81
US-09-086-663A-81
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US-09-086-663A-80
US-09-086-663A-80
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US-09-252-991A-28271
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29857, A	25380, A	7, Appli	4, Appli	11, Appl	29050, A	17311, A	20551, A	8595, Ap	6935, Ap	2, Appli	 Appli 	10120, A	993, App	278, App	20171, A	18684, A	W '75017

ALIGNMENTS

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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-02
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 8824
LENGTH: 350
TYPE: PRT
TYPE: PRT
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US-08-773-870-4
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Sequence 4, Application US/08773870
Patent No. 5912143
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8824, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS.
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

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US-09-248-796A-16753
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                                                                                                                                                                                                                                                                                                      Sequence 16753, Application US/09248796A Patent No. 6747137 GENERAL INFORMATION:
                                                                       SEQ ID NO 16753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/248,796A CURRENT FILING DATE: 1999-02-12 PRIOR APPLICATION NUMBER: US 60/074,725 PRIOR FILING DATE: 1998-02-13
                                                                                                             PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                              FILE REFERENCE: 107196.132
                                                                                                                                                                                                                                          APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                           NUMBER OF SEQ ID NOS: 28208
                 ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linea
IMMEDIATE SOURCE:
LIBRARY: GenBan
CLONE: 533511
                                                     ENGTH: 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
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PRIOR APPLICATION DATA:
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SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                     96 VVASLPLDQSDEGSSSQKEESPSTLQVLPDSESLPRSEIDEKVTDLVQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 SLSSGPL-----TOKONGLOTTEAKRDAKRMPAKEVTINVTDSIQ 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 SDAPPSAAAPDSGPEAGGLHSGMLEDGLPSNGVPRS-TAPGGIPNPEKKTNCETQCPNPQ 91
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                                                                                                                                                                                                                                  Sequence 25785, Application US/09252991A

Sequence 25785, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GOLdman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT FILING APPLICATION NUMBER: US/09/902,540
PRIOR APPLICATION: """ 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 29
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SEQ ID NO 12404
LENGTH: 656
                                                                  SEQ ID NO 25785
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                                                                                                                                                                                                FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                           PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR TILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
                                                                                           NUMBER OF SEQ ID NOS:
                           LENGTH: 208
TYPE: PRT
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ORGANISM: Pseudomonas aeruginosa
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10.8%; Score 84;
Local Similarity 26.1%; Pred. No.
hes 42; Conservative 16; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 MPAKEVTINVTDSIQQMDR-----SRRITK 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPDAGHPDACNPDAGNPDGGGPLPTVPTLIESSQSAHQVSAGQTVTFHVTGRDDLACPLQ 247
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31.5%; Pred. No. 0.48;
:ive 12; Mismatches
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Sequence 81, Application US/09086663A

Patent NO. 6518063

GENERAL INFORMATION:

APPLICANT: DUCY, PATRICIA

APPLICANT: MARSENTY, GERARD

TITLE OF INVENTION: 0SF2/CBFA1 COMPOSITIONS AND METHODS OF USE

FILE REFERENCE: UTSC:525

CURRENT APPLICATION NUMBER: US/09/086,663A

CURRENT FILING DATE: 1998-03-24

PRIOR APPLICATION NUMBER: 60/080,189

PRIOR APPLICATION NUMBER: 60/040,430

PRIOR FILING DATE: 1998-03-24

PRIOR FILING DATE: 1997-05-29

NUMBER OF SEQ ID NOS: 83
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US-09-949-016-11662
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Best Local
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SEQ ID NO 11662
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GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 507
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                                                                                                                                                                                                                                                                                                                                                            PSMRVGVPPONPRP-SLNSAPSPFNPOGOSQITDPRQAOSSP 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POSLSSGPLTQKQNGLQTTEAKRDAK---RMPAKEVTINVT 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for Windows Version
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29.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 80; DB 4;
Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-086-663A-81
                                                                                                                                                                                                                                                                                                   US-09-086-663A-71
                                                                                                                                                                                                                                                                                                                         RESULT 9
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SEQ ID NO 81
LENGTH: 521
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                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                           Sequence 71, Application US/09086663A Patent No. 6518063
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Best Local Similarity
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/086,663A
CURRENT FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/080,189
PRIOR FILING DATE: 1998-03-24
PRIOR APPLICATION NUMBER: 60/048,430
PRIOR FILING DATE: 1997-05-29
NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patentin Ver. 2.1
                                                                                                                     FILE REFERENCE: UTSC:525
CURRENT APPLICATION NUMBER: US/09/086,663A
CURRENT FILING DATE: 1998-05-29
                                                                                                                                                                               APPLICANT: DUCY, PATRICIA
APPLICANT: KARSENTY, GERARD
TITLE OF INVENTION: OSF2/CBFA1 COMPOSITIONS AND METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1997-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1998-03-24 PRIOR APPLICATION NUMBER: 60/048,430
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                                                                                                                                                                                                                                                                                                                                                                                 262 PSMRVGVPPQNPRP-SLNSAPSPFNPQGQSQITDPRQAQSSP 302
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Pred. No.
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261

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APPLICANT: DUCY, PATRICIA
APPLICANT: KARSENTY, GERARD
TITLE OF INVENTION: OSF2/CBFA1 COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 KSFTLTITVFTNPPQVÄTYHRAIKVTVDGPREPRRHRQKLDDSKPSLFSDRLSDLGRIPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 PSMRVGVPPQNPRP-SINSAPSPFNPQGQSQITDPRQAQSSP 295
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24 ESTWLTYTDSDAPPSAA-----APDSGPEAGGLHSGMLEDGLPSNGVPRSTAPGGIPN
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                                                                     Score 80; DB
Pred. No. 3.9;
                                               Mismatches
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                                                                                          DB 4; Length 528
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                                             57; Indels
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US-09-086-663A-80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: Peptide US-09-086-663A-2
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US-09-086-663A-71
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                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 29.4
                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                     Sequence 80, Application US/09086663A Patent No. 6518063
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SEQ ID NO 2
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APPLICANT: DUCY, PATRICIA
APPLICANT: KARSENTY, GERARD
TITLE OF INVENTION: OSF2/CBFA1 COMPOSITIONS AND METHODS
FILE REFERENCE: UTSC:525
CURRENT APPLICATION NUMBER: US/09/086,663A
CURRENT FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/080,189
PRIOR FILING DATE: 1998-03-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DUCY, PATRICIA
APPLICANT: KARSENTY, GERARD
APPLICANT: KARSENTY, GERARD
TITLE OF INVENTION: OSPZ/CBFA1 COMPOSITIONS;
FILE REFERENCE: UTSC:525
CURRENT APPLICATION NUMBER: US/09/086,663A
CURRENT FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/080,189
PRIOR FILING DATE: 1998-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/048,430 PRIOR FILING DATE: 1997-05-29 NUMBER OF SEQ ID NOS: 83
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                 PSMRVGVPPQNPRP-SLNSAPSPFNPQGQSQITDPRQAQSSP 370
                                                                                                                                                                                                                                                                                                                   PEKKTNCETOCPNPOSLSSGPLTOKONGLOTTEAKRDAKRMP 118
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29.4%;
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29.4%;
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Pred. No. 4.7;
7; Mismatches
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RESULT 13

US-09-949-016-7040
; Sequence 7040, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 14218
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; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14218
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US-09-902-540-14218
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PRIOR FILING DATE: 1997-05-29
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 80
LENGTH: 596
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.3%;
Best Local Similarity 24.5%;
Matches 27; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14218,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                  595 SDEASPPPGÄÄPDHGAP-----
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                                                                                                                                                                                                                                                                                                          98
                                                                                                                                                                                                                                                                                                                                                                                  31 TDSDAPPSAAAPDSGPEAGGLHSGMLEDGLPSNGVPRSTAPGGIPNP-----EKKTNCET 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 PEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 ESTWLTYTDSDAPPSAA-----APDSGPEAGGLHSGMLEDGLPSNGVPRSTAPGGIPN 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                         APPSPSPAAEDAPT----ALTALDGPVEAPPDPGMELQILSDEPYSPLER
                                                                                                                                                                                                                                                                                                        QCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAKEVTINVTDSIQQMDR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSMRVGVPPQNPRP-SLNSAPSPFNPQGQSQITDPRQAQSSP 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description of Artificial Sequence: Peptide
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Pred. No. 10;
14; Mismatches
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Pred. No. 4.7;
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                                                                             S ASSOCIATED
S OF DETECTIO
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                                                                               DETECTION AND USES THEREOF
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CURRENT PILING DATE: 1990-02-18
PRIOR APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1990-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
SEQ ID NO 21479
LENGTH: 330
TYPE: DDT
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US-09-976-594-427
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US-09-252-991A-21479
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; ORGANISM: Human
US-09-949-016-7040
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US-09-252-991A-21479
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APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. RUBENFIELD ET ALL
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                         GENERAL INFORMATION:
                                                                                                             Sequence 427, Application US/09976594 Patent No. 6673549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
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APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                                                              97
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                                                                                                                                                                                                                                                                                                                                                          86 DATPGLLPRGGGRFHRRRRDHPSPTHLPRS--PGG---KDRRLHHLRRRQAPAP---AAG 137
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                                                                                                                                                                                                                                                              PARRODPGLO 147
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FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGRAM
SEQ ID NO 427
LENGTH: 462
TYPE: PRT
ORGANIEN: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 2716815CD1
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Best Local Similarity
Matches 30; Conserva
340 SYLNGVMPPTQSFAPDPKYVSSKAL-QRQN-----SEGSASKVP 377
                                                                                     298 YRRWSAEVTSS--TYSDEDRPPK--VPPREPLS------PSNS--RTPSPKSLP
                                                                                                                                16 YESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGLPSNGVPRSTAPGGIP 75
                                          76 NPEKKTNCETO -- CPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMP 118
                                                                                                                                                                              Conservative
                                                                                                                                                                       10.1%; Score 78.5; DJ 28.6%; Pred. No. 4.7; tive 16; Mismatches
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Search completed: April 12, 2005, 15:43:29
Job time: 27.6667 secs

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Minimum
Maximum
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Maximum Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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ALIGNMENTS

R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24459
A;Rocession: T47424
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1122 <RIE>
A;Cross-references: UNIPROT:Q9M291; EMBL:AL138641
A;Cross-references: UNIPROT:Q9M291; EMBL:AL138641
A;Cross-references: Cultivar Columbia; BAC clone T22K7
C;Genetics:

hypothetical protein T22K7.20 - Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear cress) (Species: Arabidopsis thaliana (Mouse-ear cress) (C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004 (C:Accession: T47424 R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd,

Lemcke,

RESULT 1 T47424

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hypothetical protein F12G12.9 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;pate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86664
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: H86464
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A; Introns: 303/3; 363/3; 388/3; 421/3; 459/1; 501/3; 552/3; 579/3; 605/3; 636/3; 655/1;
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Local Similarity 28.4%;
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Pred. No. 10;
10; Mismatches
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RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       melanoma antigen MAGE-10 - human (,Species: Homo sapiens (man) (,Species: Homo sapiens (man) (,C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004 (,Accession: I3865) R,De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De
                                                                                                                                                           unknown protein, 45065-49536 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: A96717
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A;Cross-references: GDB:331126
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A;Molecule type: DNA
A;Residues: 1-369 <RES>
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A;Residues: 1-690 <STO>
A;Cross-references: UNI
C;Genetics:
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A;Title: Structure, chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 28
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Best Local S
Matches 33
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                                                                                                                                                                                                                                                                                                                         VVASLPLDQSDEGSSSQKEESPSTLQVLPDSESLPRSEIDEKVTDLVQ
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                                        Khaykin, E.; Kim, C
Maiti, R.; Marziali
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                                                                                                                      O.; Alonso.
: Dewar, K.
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      Tallon,
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                        99
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A;Cross-references: UNIPROT:P10637
A;Note: this sequence is inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:102045, NCBIP:102046)
R;Kenner, L.; Forstner, M.; Hutter, H.; Hoefler, G.; Kurzbauer, R.; Zatloul
submitted to the EMBL Data Library, May 1992
A;Description: First observation of mRNA for a tau-protein from murine live
A;Reference number: S31658
A;Accession: S31658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microtubule-associated protein tau mouse
N;Alternate names; microtubule binding protein tau
C;Species: Mus musculus (house mouse)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994
C;Accession: A45301; S31658
                                                                                                                                                                                                                                                                                            F;575-605/Domain:
F;606-636/Domain:
F;637-668/Domain:
                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: microtubule-associated protein tau; C;Keywords: microtubule binding; tandem repeat F;544-574/Domain: MAP2/tau repeat homology <MT1>
                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Z12133; NID:g54263; PIDN:CAA78121.1; PID:g388534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 'T', 529-651 < KEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-733 < COU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A45301;
A; Accession: A45301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Couchie, D.; Mavilia, C.; Georgieff, I.S.; Liem, R.K.; Shelanski, M.L.; Nunez, Proc. Natl. Acad. Sci. U.S.A. 89, 4378-4381, 1992
A;Title: Primary structure of high molecular weight tau present in the periphera. A;Reference number: A45301; MUID:92262443; PMID:1374898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A96712
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-860 <570>
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A;Map position: 1
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                       Local
  215
                                                                                                155 GTRPEDIEKSHPASELLRRGPPQKEGWGQDRLGSEEEVDEDLTVDESSQDSPPSQASLTP
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GRAAPQAG---SGSVCGETAS--VPGLPTEGSVPLPADFFSKVSAETQASQPEGPGTGPM
                                             G---PEAGGLHSGMLEDGLPSNGVPRSTAPGGIPNPE---KKTNCETQCPNPQSLSSGPL 98
                                                                                                                                              GSRADAIE------PRYYESWTRE-----TESTWLTYTDSDAPPSAAAPDS 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NTGTN--TGMPN-----SNGMPTSSS 176
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                                                                                                                                                                                                                                                                                         MAP2/tau repeat homology <MT2>
MAP2/tau repeat homology <MT3>
MAP2/tau repeat homology <MT4>
                                                                                                                                                                                                                     10.9%;
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Pred. No. 11;
9; Mismatches
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                                                                                                                                                                                                                     Score 84.5;
Pred. No. 1
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                                                                                                                                                                                                                                         Length 733;
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                                                                                                                                                                                              31;
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RESULT 6
W2WLDP
E2 protein -
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable ppp protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Date: 17-Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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A;Status: preliminary; nucleic acid sequence not
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A;Residues: 1-416 <GRO>
C;Superfamily: papillomavirus E2 protein
C;Keywords: early protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Groff, D.E.; Lancaster, W.D.

J. Virol. 56, 85-91, 1985

A;Title: Molecular cloning and nucleotide sequence of deer papillomavirus.

A;Reference number: A93013; MUID:85293253; PMID:2993669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: host Odocoileus virginianus (American white-tailed deer) C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change C;Accession: A03673
                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues:
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Best Local (
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;35-243/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: UNIPROT:P71588; Experimental source: strain H37Rv
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Species: deer papillomavirus
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Best Local Similarity 31.7%;
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457
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                                                                                                                                                                                                                                                                          Similarity
----SPTTSAPAPTGTTPA
                                       KONGLOTTEAKRDAKRMPA 119
                                                                                 AGTLDDAIGQLRELAANSLLPPCPAPRATSPPGRPAP--PTTSETTEPNVTSSPASP---
                                                                                                                                                                     MGC-----LSPR--
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ilarity 25.9%;
Conservative 1
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Pred. No. 9.6;
10; Mismatches
                                                                                                         LPSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQ 100
                                                                                                                                                                ---NELSQISYGQSGGPLDCHLMKLEDLRPPERAQVRAGLP
471
                                                                                                                                                                                                                                                                        Score 84; DB 2;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                       GB: Z80233; GB: AL123456; NID: g3261645; PIDN: CAB02438
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A;Gene: crtA
C;Superfamily:
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RESULT 10
IJMSNL
neural cell adhesion
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C;Species: Rhodobacter sphaeroides
C;Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-672 <FIN>
A; Cross-references: UNIPROT: Q45343;
A; Experimental source: strain 18323
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Mol. Microbiol. 16, 625-634, 1995
A;Title: Tracheal colonization factor: a Bordetella pertussis secreted virulence
A;Reference number: 140333; MUID:96065692; PMID:7476158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Bordetella pertussis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: S77633; I40333
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A; Residues: 1-327 < LAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tracheal colonization factor A precursor - N_iAlternate names: tcfA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F_11-39/Domain: signal sequence #status predicted <SIG> F_140-672/Product: tracheal colonization factor A #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                        Best
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                   190 GAGGPHGEAIKAVRAENWFKEELYARFQILGTIGKWEGKDPVGEALTARPSEAPKPAPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 HKDNPSPPVVGVGPGMAESSGGHNPGVGGGTHENGLPGIGKVGGSAPGPGGLGRNDENSE
                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 YTDSDAPP----SAAAPDSGPEAGGLHSGMLEDGLPSNGVPRSTA--PGGI----PNPE 78
                                                                                                                                                                                                                                                                                                                         2 GCGGSRADAIEPRYYESWTRE----TESTW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S77633
                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                         DSGPEAGGLHSGMLEDGLPSNGVPRSTAPGGIPNP-EKKTNCETQCPN----PQSLSSGP
                                                                                                             KPFRSRGLEADAAGREAE
                                                                                                                                                   LTQKQNGLQTTEAKRDAK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSLNPGTLGPSPGPDTSTGSGPDAGMASGAGSTSPGASGGAGKDA--MPPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKTNCETQCPNP----QSLSSGPLTQKQNGLQTTE-----AKRDAKRMPAKE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                       spheroidene monooxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNIPROT:Q54790; EMBL:X82458;
                                                                                                                                                                                                                                                                                                                                                                                        10.7%; Score 83.5; 23.9%; Pred. No. 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.8%; Score 84; 31.2%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                  15,
                                                                                                             310
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                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                  PAAEAPKPAPAPVAEKPALAVEMPKPAEPPKPVVEAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bordetella pertussis
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                                                                                                                                                                                                                                                                                                                            ----LTYTDSDAPPSAAAP
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molecule

μ.

precursor,

long domain splice

Form

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A;Map position: 9

A;Introns: 643/3; 701/1; 770/2; 809/2; 1076/2

C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu C;Superfamily: neural cell adhesion; cell adhesion; duplication; heparin binding; si C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1115/Product: neural cell adhesion molecule, long domain splice form #status experi
                                                                                                                                                                                                                                                                                                                                                                                                                       F;132-191/Domain: immunoglobulin homology <IMM2>
F;132-156/Region: heparin binding #status predicted
F;151-165/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-290/Domain: immunoglobulin homology <IMM3>
F;262-272/Region: NCAM binding #status predicted
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A;Residues: 529-809,107-1115 <SAN>
A;Residues: 529-809,107-1115 <SAN>
A;Coss-references: EMBL:X06328; NID:g53322; PIDN:CAA29641.1; P
R;Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A;Title: Differential splicing and alternative polyadenylation A;Reference number: S00382; MUID:88283628; PMID:3396534
A;Accession: S00384
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-548, 'T',550-571, 'T',573-574, 'D',576-588, 'MQPS',593, 'S',595-599,'P',601,'L'
A;Cross-references: UNIFROT: P13595; EMBL: Y00051; NID: 953342; PIDN: CAA68263.1; PID: 953343
A;Cross-references: UNIFROT: P13595; EMBL: Y00051; NID: 953342; PIDN: CAA68263.1; PID: 953343
R;Santoni, M.J.; Barthels, D.; Barbas, J.A.; Hirsch, M.R.; Steinmetz, M.; Goridis, C.; W
Nucleic Acids Res. 15, 8621-8641, 1987
Nucleic Acids Res. 15, 8621-8641, 1987
A;Title: Analysis of CDNA Clones that code for the transmembrane forms of the mouse neurl
A;Reference number: S00844; MUID: 88067687; PMID: 3684567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain splice form (NCAM-140 C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text change 09-Jul-2004
C;Accession: A29673; S00844; S00384; A28281; A44290; S00383
R;Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M. EMBO J. 6, 907-914, 1987
EMBO J. 6, 907-914, 1987
A;Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for A;Reference number: A29673; MUID:87246524; PMID:3595563
                                                                                                                                                                                                                                                                       F;625-685/Domain:
                                                                                                                                                                                                                                                                                                           F;519-596/Domain:
                                                                                                                                                                                                                                                                                                                                                   F;420-482/Domain:
                                                                                                                                                                                                                                                                                                                                                                                               F;323-388/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A28281
A;Molecule type: mRNA
A;Residues: 804-1081 <BA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Batthels, D.; Vopper, G.; Wille, W.
Nucleic Acids Res. 16, 4217-4225, 1988
Nucleic Acids Res. 16, 4217-4225, 1988
A;Tille: NCAM-180, the large isoform of the neural cell adhesion molecule of the mouse,
A;Reference number: A28281; MUID:88247737; PMID:2454455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;34-98/Domain: immunoglobulin homology <IMMl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Structural and immunological characterization of A; Reference number: A44290; MUID:86140120; PMID:3512556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Rougon,
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A;Accession: A28281
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A;Residues: 642-1115 <BAR>
A;Cross-references: EMBL:X07195
                                                                                                                                                                                                                           ;519-596/Domain: fibronectin type III repeat homology <FN3A>;625-685/Domain: fibronectin type III repeat homology <FN3B>;712-729/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                   730-1115/Domain: intracellular #status predicted <INT>
741-96,139-189,235-288,330-386,427-480/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Gene: NCAM
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol;Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IJMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: EMBL:X07244; NID:g53321; PIDN:CAA30230.1; Rougon, G.; Marshak, D.R. Biol. Chem. 261, 3396-3401, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contains: neural cell adhesion molecule, short domain splice form (NCAM-140); Species: Mus musculus (house mouse)
Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text change 09-Jul-2004; Accession: A29673; S00844; S00384; A28281; A44290; S00383; A29673; S00844; Molecular Molecular A29673; S00844; S00384; A28281; A44290; S00383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-711/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: A44290
                                                                                                               316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                   immunoglobulin homology <IMM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <ROU>
   10.7%;
   Score
Pred.
   No. 33;
                                       DB
                                       <u>;</u>
                                   Length 1115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:g929720
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                                                                                                                   #status
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                                                                                                                   predicted
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A; Residues: 1-1366 <MUR>
A; Cross-references: UNIPROT: Q92529;
A; Cross-references: strain A3(2)
                                                                                                                                                                                                                                                                                                                                               C;Accession: T35985
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, submitted to the EMBL Data Library, February 1999
                                                                                                                                                                                                                                                                                                                                                                                              probable large Pro/Ala/Gly-rich protein - Streptomy C; Species: Streptomyces coelicolor C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
밁
                                                                                                                                                                                                    A;Gene:
                                                                                                                                                                                                                                                                                                                    A; Reference number: Z21589
A; Accession: T35985
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                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from
                                                                                                                                Query Match
Best Local S
Matches 33
                                                                                                                                                                                                                  Genetics
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                                                                                                                                                                                                    SCOEDB:SC9F2.06c
                                                                458
500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        941 PASKASPAPTPT 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          882 TASSSSPASAPKVAPLVDLSDTPTSAPSASNLSSTVLANQGAVLSPSTPASAG-ETSKAP 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         830
                                                                                                                                                                                                                                                                                                                                                                                                                     srge Pro/Ala/Gly-rich protein - Streptomyces coelicolor
Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 -PRSTAPGGIPNPE---KKTNCETQCPNPQSLSS-----
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                                                                                                                                  33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 SRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGLPSNGV
                                                                                                                                                Similarity
GTGLRGSGTVAAGGVPLFGARGGVSGAAGGVPLPTVFTASEPR-PGP
                           --GMLEDG-LPSNGVPR-----STAPGGIPNPEKKTNCETQCPNP
                                                                   GAGAARR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNSDTITETFATAQNSPTSET-TTLTSSIAPPATTVPDSNSVPAG-
                                                                                                 GCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPD--SGP----EAGGLHS- 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDAKRMPAKEVT
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                10.6%;
                                                                  ---PTWAKEAPS
                                                                                                                                  12;
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                                                                                                                                Score 82.5; DI
Pred. No. 51;
L2; Mismatches
                                                                                                                                                                                                                                                   EMBL: AL035559; PIDN: CAB37473.1; GSPDB: GN00070; SCOED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                    GB/EMBL/DDBC
                                                                                                                                                                   DB
                                                                PPASTAPEPWSGPGGAVGEAGGVSSP
                                                                                                                                  25;
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                                                                                                                                                                                                                                                                                                                                                                    J.; Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                  #text_change 09-Jul-2004
                                                                                                                                                                Length 1366;
                                                                                                                                  Indels
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A; Decide type: DNA
A; Residues: 31-318 < DUI2>
A; Residues: 31-318 < DUI2>
A; Cross-references: EMBL: X60468; NID: 957561; PIDN: CAA42998.1;
A; Cross-reference was submitted to the EMBL Data Library,
                                                                           A;Introns: 88/3; 107/3; 135/3; 157/3; 207/3; 250/2; C;Keywords: transcription regulation F;42-78/Domain: WW repeat homology <WW1>
                                                                                                                                                                                                                                                                                                                                                                                               R;Duilio, A.; Zambrano, N.; Mogavero, A.R.; Ammendola, R.; Cimino, F.; Russo, T. Nucleic Acids Res. 19, 5269-5274, 1991
A;Title: A rat brain mRNA encoding a transcriptional activator homologous to the A;Reference number: S22571; MUID:92020215; PMID:1923810
A;Accession: S22571
                                                                                                                                                                                                                                                                              A;Status: nucleic
                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q99MK3; A;Accession: S22572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004 C;Accession: S22571; S22572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  integrase-like protein FE65 - rat
C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-499 < DUI1>
                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
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       Query Match
Best Local Similarity
                                                                                                                                                    Genetics:
                                                                                                                                                                                                                                                                            acid sequence not
          10.5%;
25.3%;
          Score 81.
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19;
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                                   Length 499;
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1-2806 <STO>
A;Rosidues: 1-2806 <STO>
A;Cross-references: UNIPROT:Q8X470; GB:AE005174; NID:g12514354; PIDN:AAG55616.1; GSPDB:
A;Experimental source: strain O157:H7, substrain EDD933
C;Genetics:
                                                                                                                                                                                                                                                                                                        C;Accession: D85644
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glass iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, Nature 409, 529-533, 2001
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                                                                                                                                                                                                                                                                         A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein Z1495 [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli (c;Species: Becherichia coli (c;Species: Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: D85644
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A;Residues: 1-2793 <HAY>
A;Cross-references: UNIPROT:Q8X2Q2; GB:BA000007; PIDN:BAB34665.1; PID:g13360702; GSPDB:A;Experimental source: strain O157:H7, substrain RIMD-0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B90784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Hayashi, T.; Makino, K.; Ohnishi,
gasawara, N.; Yasunaga, T.; Kuhara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein ECs1242 [imported] - C;Species: Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSSGPLTQKQNGLQTTEAKRDA---KRMPAKEVTINVTDSIQQMDRSRRI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPSAAAPDSGPEAGGLHSGMLEDGLPSNGVPRSTAP--GGIPNPEKKTNCETQCPNPQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LHSGMLEDGLPSNGVPRSTAPG--GIPNPEKKTNCETQCP-NPQSLSSGPLTQKQNGLQT 107
APPSAAAPDSGPEAGGLHSGMLEDGLPSNGVPRSTAP--GGIPNPEKKTNCETQCPNPQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEAKRDAKRMPAKEV-TINVTDSIQQMDRSRRITKNCV 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNAFETDSDLPAGWMRVQDTSGTYYWHIPTGTTQWEPPGRASPSQGNSPQEESQLTWTGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRYYES-----WTR--ETESTWL----TYTDSDAPPSAAAPDSG--PE-----AGG
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Pred. No. 1.4e+02;
                                                         Score 81.5;
Pred. No. 1
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                                        Mismatches
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                                    ; DB 2;
1.4e+02;
hes 54;
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lanta, E.;
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K.; Ag
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Apodaca,
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translation initiation factor-like protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: A85359 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999
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A;Molecule type: DNA
A;Residues: 1-263 <STO>
Search completed: April 12, Job time : 23.6667 secs
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                                                                                                                             118 PAKEVTINVTDSIQQ 132
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                                                                                                                                                                        58 ALVQGNG---SQQPKPVPSPTRQT-VEKPKPQPQPQEVAPPT--TTSLNTVELSRKTNSL
                                                                                                                                                                                                                 60 -- LPSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRM
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Similarity 28.1%;
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2: uniprot_trembl:*
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Q73w33
Q828t2
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Q6c2r4
Q6fkp2
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Q8wne8
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11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.3	11.3	11.3	11.3	11.4	11.4	11.4
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RX PubMed=14702039; DOI=10.1038/ng1285; RX PubMed=14702039; DOI=10.1038/ng1285; RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Fujimori K., RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Fujimori K., RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Fujimori K., RA Alomiya K., Takiguchi S., Watanabe M., Hiraoka S., Chiba Y., Ishida S., RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S., RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S., RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Gunori Y., RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okama M., Pujiwata T., RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., RA Matsumura K., Nagase T., Nomura N., Kikuchi H., Msuho Y., Yamashita R., RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., Tonglete sequencing and characterization of 21,243 full-length human 01-MAR-2001 01-MAR-2001 25-OCT-2004 Q9НА93 Q9НА93; MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498; Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., "Complete sequencing CDNAs."; Eukaryota; Metazoa; Mammalia; Eutheria; leukemia, c Name=BAALC; Hypothetical SEQUENCE FROM N.A. TISSUE=Whole embryo; SEQUENCE FROM N.A. NCBI_TaxID=9606; Homo sapiens (Human) Genet. cytoplasmic) (TrEMBLrel. 16, Created) (TrEMBLrel. 16, Last sequence update) (TrEMBLrel. 28, Last annotation update) 1 protein FLJ12015 (BAALC isoform 1-6-8) ytoplasmic) (BAALC 1-6-8). 36:40-45 (2004). PRELIMINARY; Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo. PRT; 145 ₿ (Brain and acute

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WA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rak Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Tones S.J. Marya M.A.;
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EMBL; AF371319; AAL50515.1; -.
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EMBL; AF363578; AAL50377.1; -.
InterPro; IFR009728; BAALC N; Ifferm; PF06989; BAALC N; I.
SEQUENCE 145 AA; I5551 MW; C
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tive 0; Mismatches 0;
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SEQUENCE FROM N.A.

MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;

"BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia."; proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).

EMBL; AF77132; AALS0518.1; -.

Pfam; PF06989; BAALC.N; 1.

SEQUENCE 145 AA; 15401 MW; C75ED7D00BF82E26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8WNE9;
01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498; Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinoner Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; "BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia."; Proc. 90, 187363578; AAL50379.1; -. SMBL; AF363578; AAL50379.1; -. Pfam; PF06889; BAALC_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAR-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
BAALC isoform 1-6-8.
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                                                                                                                             MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
EVTINUTESIRQUDRNQRITKKCIN
                    EVTINVTDSIQQMDRSRRITKNCVN 145
                                                      SANGVPRSTAPGGTSNPEKKMSCGTQCPNPQSLGSGPLTQKQNGLRTTEAKRDAKRTSAK
                                                                               PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK
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Pred. No. 7.8
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RESULT Q8VHV1

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STRAIN=C57BL/6J; TISSUE=Cerebellum;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Yamamoto R., Matsumoto H., Sakaguchi S., Hegami T., Kashiwagi K.,

Yujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-Cerebellum;

MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genome Res. 10:1617-1630(2000).
                    STRAIN=C57BL/6J; TISSUE=Cerebellum;
Adachi J., Aizawa K., Akimura T., Arakawa T
Fukuda S., Furuno M., Hanagaki T., Hara A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Cerebellum; MEDLINE=99279253; PubMed=10349636; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA c Meth. Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=21085660; PubMed=11217851;
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
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Mammalia; Eutheria;
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T-2004 (TrEMBLrel. 28, Last annotation update)
isoform 1-6-8 (Mus musculus 16 days neonate cerebellum cDNA,
full-length enriched library, clone:9630028H16 product:brain
leukemia, cytoplasmic, full insert sequence).
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Rodentia;
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Sciurognathi; Muridae;
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A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.
A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (ApR-2002) to the EMBL, AG731320; AAL50516.1; -.
R EMBL; AK079337; BAC37611.1; -.
R EMBL; AK07937; BAC37611.1; -.
                                                                                                           "BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopolesis and acute leukemia."; Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).

EMBL; AB073318; BAB70507.1; -.
EMBL; AF371321; AAL50517.1; -.
Pfam; PF0898; BAALC.N; 1.
Pfam; PF0898; BAALC.N; 1.

D5A27AD67456F341 CRC64;
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Q920K5;
Q1-DEC-2001 (TrEMBLrel. 19, Creat
Q1-DEC-2001 (TrEMBLrel. 19, Last
Q1-DEC-2004 (TrEMBLrel. 27, Last
Dem-A20-4 (BAALC isoform 1-6-8).
                                                                                                                                                                                                             Tanner S.M., Austin J.L., Leone G., Rush L.J., Plas Mrozek K., Sill H., Knuutila S., Kolitz J.E., Arche Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                    Name=dem-A20-4; Synonyms=Baalc; Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
Wang X., Tian
                                                                                                                                                                                                                                                    STRAIN=Sprague-Dawley;
MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2810457D07 product:brain and acute leukemia,
cytoplasmic, full insert sequence.
                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636;
                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
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EMBL; AF363578; AAL50381.1; -.
Genew; HGNC:14333; BAALC.
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CSTRAIN=(579EL/63); TISSUE=Whole body;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=110.76861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=110.1150/8861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=110.1150/8861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=110.1150/8861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=110.1101/gr.152600;

MEDLINE=20530913; PubMed=10.1101/gr.152600;

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A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
A Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Sogabe Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
A Muramatsu M., Hayashizaki Y.,
A Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

B MGD., MGD.
                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local :
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STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=20499774; PubMed=11042159; DOI=10.1101/gr.145100;
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STRAIN=C57BL/6J; TISSUE=Whole body;
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Meth. Enzymol. 303:19-44(1999).
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91
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                                                DAKRMPAKEVTINVTDSIQQMDRSRRITKNCVN
                                                                                                                                                                                                                                        SGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKR 112
DAKRMSAREVAINVTENIROMDRSKRVTKNCIN
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Pred. No. 2.9e-23;
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Hori F.,
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Sakai K.,
Niraki T.,
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RN 121

RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC TISSUB-Brain;

RX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Pahey J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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AC Q880
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Best Local
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
BAALC isoform 1-8 (BAALC protein) (BAALC 1-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498; Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heino: Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; "BAALC, the human member of a novel mammalian neuroectoderm ge: lineage, is implicated in hematopoiesis and acute leukemia."; proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Pfam;
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SEQUENCE FROM N.A.

MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heino
Tanner S.M., Austin J.L., Kolitz J.E., Archer K.J.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-MAR-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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PF06989; BAALC N; 1.
NCE 73 AA; 7871 MW; 9
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Primates;
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1; Mismatches
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, Last sequence up
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(TrEMBLrel.

200

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Name=BAALC; Sus scrofa

Metazoa;

Chordata;

Craniata; Vertebrata;

Euteleostomi;

(Pig)

BAALC isoform 1-8.

Q8WNE8; Q8WNE8; 01-MAR-2002 01-MAR-2002 01-MAR-2004

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Best Local S
Matches 53
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Best Local S
Matches 54
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                                                                                                                                                                                                                                                                                                                                          Q8WXS2;
Q8WXS2;
01-MAR-2002
01-MAR-2002
01-MAR-2004
                                                                                                                                     MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498; Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinoner Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; "BAALC, the human member of a novel mammalian neuroectoderm gene "Ineage, is implicated in hematopoiesis and acute leukemia."; Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).

EMBL; AR363578; AAL50382.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones S.J., Marra M.A.; "Generation and initial analysis of and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:160
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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Rodriguez A.C., Grimwood
Krzywinski M.I., Skalska
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                                                                                                                            80 AA;
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                                                                              37.7%; S. larity 100.0%; | Conservative 0;
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Primates;
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S. S.
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Last sequence update)
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, Schmutz J., My
, Smailus D.E.,
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Pred.
                                                                                                   Score 293;
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                                                                                                                              70BE9B91C3245E2D CRC64;
                                                                               Pred. No. 2.;
Mismatches
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, Myers R.M., But
E., Schnerch A.,
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RESULT 13
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DT 05-JU
DT 05-JU
DT 05-JU
CS BAALC
GN Name=
OC Rattu
OC Eukar
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Best Local S
Matches 51
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Best Local S
Matches 51
                                                                                                                                                                                                         Q790N3;
Q790N3;
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21574584; PubMed-11707601; DOI=10.1073/pnas.241525498; Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinor Mrozek K., Sill H., Knuuttila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; "BAALC, the human member of a novel mammalian neuroectoderm generates, is implicated in hematopoiesis and acute leukemia."; Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
EMBL; AR371324; BAAL50520.1; -.
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EMBL; AF371326; AALLC N; 1.

Pfam; PPO6899; BAALC N; 1.

ESQUENCE 54 AA; 5681 MW; 6538C3DABED98825 CRC64;
   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                              BAALC isoform 1-8.
                                                                                                                                                                              05-JUL-2004
                                                                                                               Name=Baalc;
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01-MAR-2002
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Mammalia; Eutheria;
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NCE 54 AA; 5667 MW;
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(TrEMBLrel.
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Rodentia;
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94.4%;
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94.4%;
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; Pred. No. 2.2e:
1; Mismatches
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Pred. No. 1e-1
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEE8C0EBFBCDB829 CRC64;
   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                              PRT;
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annotation update)
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Q801V5;
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2003 (TrEMBLrel. 26, Last annotation updats SI:zC215113.3 (Novel protein similar to human bra leukemia, cytoplasmic (BAALC)) (Fragment).
                                               Hypothetical protein.
OrderedLocusNames=TTC1434;
Thermus thermophilus (stra
                                                                                  05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Sprague-Dawley;

MEDLINB-21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinor Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,

Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;

"BAALC, the human member of a novel mammalian neuroectoderm ger lineage, is implicated in hematopoiesis and acute leukemia.";

Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
                                                                                                                        Q72HQ2;
                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                 Pfam; PF
NON_TER
                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases EMBL; AL807244; CAD87801.1; -. Interpro; IPR009728; BAALC_N.
                                                                                                                                                                                                                                                                                                                                                                                                                               Actinopterygii; Neopterygii; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leukemia, cytoplasmic Name=SI:zC215I13.3;
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Pfam; PF06989; BAALC N; 1.
SEQUENCE 54 AA; 5667 MW;
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Metazoa; Chordata; Craniata; Vertebrata;
gii; Neopterygii; Teleostei; Ostariophys:
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27,
27,
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Last
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Pred. No. 2.2e
1; Mismatches
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Pred. No. 3.1e-06;
1; Mismatches 2
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                                                                                   sequence update)
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Ostariophysi; Cypriniformes;
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NCBI_TaxID=262724; [1]

Thermus.

Bacteria; Deinococcus-Thermus;

(strain HB27

B27 / ATCC BAA-163 / DSM 7039).
Deinococci; Thermales; Thermac

Thermaceae;

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RP SEQUENCE FROM N.A.

RX PubMedel5064768;
RA Henne A., Brueggemann H., Raasch C., Wiezer A., Hartsch T.,
RA Lieseggang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Lieseggang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Lieseggang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
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RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Lienard T., Gohl O., Martinez-Arias R.,
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Minimum DB
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Human hea Human dia Human pol Horsophil Drosophil	Aay24750	Abo69719	Abg15607	Abg09899	Adj37991	Abb58571	Aau76758	Abj17935	Abb61076	Aaw01884	Aaw01875			Aam42082	Aam42081	Aam40295	Aam40296	Abm83972	Adi40859	Adj70139
		Pseudomon	Novel hum	Novel hum	D melanog	Drosophil	Novel rec	Drosophil	Drosophil	Invertebr	Neuronal	Novel hum	Antagonis			_	_	Human	Human	Human

AD048479; ADO48479 standard; protein; 145 8

ALIGNMENTS

PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; mouse; murine.

Mouse PTH responsive gene protein.

12-AUG-2004 (first entry)

Mus sp.

WO200404152-A2

27-MAY-2004.

10-NOV-2003; 2003WO-US035655

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12-NOV-2002; 2002US-0425532P

(AMHP) WYETH

Robinson JA, Stojanovic-Susulic V, Babij P, Murrills

WPI; 2004-420299/39. N-PSDB; ADO48478.

New nucleic acid fragment encoding a PAIGB polypeptide, useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis.

Claim 9; SEQ ID NO 8; 169pp; English.

The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the chimeric construct; a vector comprising the nucleic acid fragment; obtaining a nucleic acid fragment encoding the polypeptide; a method for obtaining a polypeptide; detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody; an agent that alters the expression of PAIGB gene or polypeptide;

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RESULT 2
ADO48473
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Best Local Similarity
WPI; 2004-420299/39
N-PSDB; ADO48472.
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                                                                                                                         Robinson JA, Stojanovic-Susulic V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTH responsive gene; PAIGB; bone-forming; bone; bone density modulation; transgenic animal; osteopathic; gene therapy; osteoporosis; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat PTH responsive gene protein.
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                                                                                                                                                                                                                                                                                                   12-NOV-2002; 2002US-0425532P
                                                                                                                                                                                                                                                                                                                                                                                        10-NOV-2003; 2003WO-US035655
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CC fragment; an antibody that specifically binds to one or more epitopes of in a mammal comprising the nucleic acid fragment, polypeptide; a composition for regulating bone-forming activity in a mammal comprising the expression of PAIGB gene or polypeptide; a composition of PAIGB gene or polypeptide; a card fragment, polypeptide; an agent that alters the expression of PAIGB mRNA; cc determining agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related cd disorders; evaluating the efficacy of a treatment of a bone related cd disorders; evaluating the effectiveness of treatment of a subject with a bone related given the study of bone density modulation comprising the DNA; an animal model companies composed of the transgenic animal comprising the modulation of bone mass; studying bone mass determinants; studying the modulation of bone dass; studying an effect of PAIGB on bone disorders; identifying an agent for treating bone related disorders; identifying whether an agent which has bone forming activity; and a stably transfected cell line comprising two constructs, the first construct comprising a ligand binding domain clinked to a DNA binding domain which is linked to an activation domain construct comprising multiple copies of DNA binding elements linked to a construct composition for paige gene is induced. The PAIGB polynucleotide has osteopathic activity. The PTH responsive gene may be related disorders, e.g., osteoporosis. This sequence represents a PTH cresponsive gene protein of the invention.
                                                                                                                                                                                                                                                                                                                                                    Matches 141;
                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                               Sequence 145 AA;
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                                                                                                                                                                                                                Local Similarity
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MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGP
                                                                                                                                                                            Conservative
                                                                                                                                                                                                            97.3%;
                                                                                                                                                                       2;
                                                                                                                                                                       Score 746; DB 8; Length 145; Pred. No. 6.6e-76; Mismatches 2; Indels
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RESULT 3
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                                                                            AAB95018;
                        Human protein sequence SEQ ID NO:16726.
                                                                                                    AAB95018 standard;
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                                                                                                                                                                                   EVAINVTENIRQMDRSKRVTKNCIN 145
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                                                                                                                                                                                                                     SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQSLSSGPLTQKQNGLWTTEAKRDAKRMSAR
                                                 (first entry)
                                                                                                    protein;
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Human; primer; detection; diagnosis; antisense therapy; gene therapy.

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Best Local S
Matches 121
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                               sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotide; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                  Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 fullength cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
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                                                                                                                                                                                                                                                                                                                    present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HELI-) HELIX RES INST.
                                                                                                                                                                                                                             Local Similarity
121
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                    EVAINVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                            MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
                                                                  PSNGVPRSTAPGGI PNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK
                                                                                                                                        MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                              Conservative
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2000JP-00183767.
2000JP-00241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                             84.6%;
                                                                                                                                                                                                           ; Score 649; DB 4;
; Pred. No. 6.3e-65;
10; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashi K,
A, Nagai K,
 145
                                                                                                                                                                                                            14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Otsuki
                                                                                                                                                                                                                                              Length 145
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                            0
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602 full-
and/or
                                                                                                     120
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RESULT 4 AAO19498

RESULT 5
ABR58646
ID ABR5
XX
AC ABR5
XX
DT 09-J

ABR58646 standard;

protein;

145

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ABR58646;

09-JUL-2003

(first entry)

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                                                                                                                                                                        Matches 121;
                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                       The present invention relates to the use of expressed sequence tags (RSTB), or variants, of the unigene cluster HS169395 (HS1), HS127144 (HS2) and/or HS132793 (HS3) for diagnosis and therapy of tumours, in which their expression rates in tumour cells and/or lymph nodes are determined. The EST sequences are useful as prognostic markers of survival of cancer patients (high levels of EST-related mRNA are associated with a poor prognosis, specifically correlated with development of metastases); and for diagnosis and/or therapy of solid tumours, particularly of colon, stomach and breast. The present sequents a variant of the HS1 protein shown in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosis and therapy of tumors, specific expressed sequence tags blocking their expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HS1; variant; cancer; tumour; unigene cluster; cytostatic; EST; expressed sequence tag; colon cancer; stomach cancer; HS169395; HS127144; HS2; HS132793; HS3.
                                                                                                                                                                                                                                Sequence 145
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brett D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JAN-2001; 2001DE-01003694.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JAN-2001; 2001DE-01003694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DE10103694-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HS1 protein variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAO19498 standard; protein; 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN
                                                                                                                                                                                       Match 84.6%;
Local Similarity 83.4%;
  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002-644836/70
                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Page 5; 10pp; German
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                                                                                                                                           MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
EVTINVTDSIQQMDRSRRITKNCVN 145
                                                                                   SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAR
                    EVAINVTENIROMDRSKRVTKNCIN 145
                                                           PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK
                                                                                                                  MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kemmner W;
                                                                                                                                                                           Conservative
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                                                                                                                                                                      10;
                                                                                                                                                                        Score 649; DB 5;
Pred. No. 6.3e-65;
0; Mismatches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             determining expression rates of the unigene cluster, and subsequently
                                                                                                                                                                                                    Length 145;
                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metastasis;
breast canc
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the
                                                                                                                                                                        Gaps
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                                                                                       120
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cc related gene nucleotide sequences which encode the proteins given in Cc ABR59521 to ABR59709. Also described: (1) determining the presence or cc absence of a pathological cell in a patient; (2) an expression vector cc comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by cc comprising the vector; (4) an isolated polypeptide, which is encoded by cc comprising the vector; (4) an isolated polypeptide, which is encoded by cc comprising the vector; (4) an isolated polypeptide, which is encoded by cc of (4); (6) specifically targeting a compound to a pathological cell in a cc patient by administering to the patient the antibody above; and (7) a cc drug screening assay. The nucleic acid is useful as diagnostic markers or therapeutic targets. In particular, the nucleic acid is useful for cd diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, cc diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, cc bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, cc pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in contact of the contact of the second contact of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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13-NOV-2001; 2001US-0350666P.
08-FEB-2002; 2002US-035515P.
08-FEB-2002; 2002US-0355257P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Afar D,
Zlotnik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1031 genes up-regulated in acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New genes that are up-regulated or down-regulated in cancers, useful markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cancer related protein SEQ ID NO:303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes an isolated nucleic acid molecule, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Page 753; 767pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-SEP-2002; 2002WO-US029560
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)B; ACC72796.
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                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOB
                                                                        EVAINVTENIROMDRSKRVTKNCIN 145
                                                                                                                                                        PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK
                                                                                                                                                                                                                                 SSNGVLRPAAPGGIANPEKKWNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAR
                                                                                                                                                                                                                                                                                                             MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSGMLEDGL
                                                                                                                                                                                                                                                                                                                                                          MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
EVTINVTDSIQQMDRSRRITKNCVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 649; DB 6;
Pred. No. 6.3e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mack DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT 6
ADC31800
                                                                                                                                                                                                                                                                                                                                            molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostation
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's diseaseneurodegenerative diseases; anaemia; platelet disorder; wound;
                                                     24-SEP-2001; 2001US-0324631P
                                                                                                       24-SEP-2002; 2002WO-US030474
                                                                                                                                                                                                              WO2003029271-A2
                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                gene therapy; chromosome 8.
                                                                                                                                                                                                                                                                                                                                                                                                                               ulcers; osteoporosis; autoimmune disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADC31800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC31800 standard; protein;
(HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence,
                                                                                                                                                                                                                                                                                                                                              immunosuppressive; antiinflammatory; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO:1882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           burns;
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New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or

Tang Zhou

Y,

Zhang J, Ghosh M,

J, Ren F, Xt M, Wang D, Ma , Drmanac RT;

Xue AJ, Ma Y, A

, Zhao QA, Asundi V,

Wang Wang J, Wang Z,

Wehrman T; Weng G;

'n

20; SEQ ID NO 1882; 1185pp; English.

The invention relates to 971 novel human cDNA sequences (ADC29919-CC ADC30889) and the polypeptides they encode (ADC30899-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of collecting of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or andlorating a medical condition, kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention; methods for the identification of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 contic semences corresponding to the countries of the invention. contig sequences corresponding to the cDNA sequences of the invention (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628 - ADC3394). The nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, anaemia, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptic polypeptides

음 성 밁 Ş 밁 δ

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RESULT 7
ADM46959
ID ADM4
XX ADM4
AC ADM4
AC ADM4
XX ADM4
AC ADM4
XX ACUT
KW ACUT
KW CYTC
CXW CYTC
CXW CYTC
CXW CYTC
CXX HOMC
XX HOMC

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The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful
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                                                                                                                                                                                                                                     Characterizing acute or chronic myelogenous leukemia, of in a patient comprises assaying for the overexpression BAALC transcripts in cells obtained from the patient.
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chronic myelogenous leukemia
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                                                                                                                                                                                    Disclosure;
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Pred. No. 6.3e-65;
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The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the chimeric construct; a vector comprising the mucleic acid fragment; obtaining a nucleic acid fragment encoding the polypeptide; a method for obtaining a polypeptide; detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide or antibody; an agent that alters the expression of PAIGB gene or polypeptide; determining whether an agent alters the expression of pAIGB mRNA; acceeding agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid fragment encoding a PAIGB polypeptide, useful preparing a composition for diagnosing, treating or preventing related disorders, e.g., osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murrille
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RESULT 9
ADM46961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC disorders; evaluating the efficacy of a treatment of a bone related CC disorder in a subject; identifying polypeptides capable of binding to CC PAIGB; monitoring the effectiveness of treatment of a subject with a bone CC related agent; a transgenic animal comprising the DNA; an animal model CC for the study of bone density modulation comprising a first group of CC animals composed of the transgenic animal and a second group of control CC animals; studying bone mass determinants; studying the modulation of bone CC mass, studying an effect of PAIGB on bone disorders; identifying an agent which has bone forming activity; and a stably transfected cell line comprising CC linked to a DNA binding domain which is linked to a DNA binding domain which is linked to a DNA binding domain which is linked to an activation domain CC all of which expression is driven by a constitutive promoter, the second CC minimal promoter which is linked to PAIGB cDNA, where upon the addition of chemical inducer, transcription of PAIGB cDNA, where upon the addition of composition and treat disorders by gene therapy. The pTH responsive gene may be constitued disorders, e.g., osteoporosis. This sequence represents a PTH CC responsive gene protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Simi
Matches 121;
                                                                           09-NOV-2001; 2001US-0348210P
                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                       Cytoplasmic; exon.
                                                                                                                                                                                                                                                                                                                                     acute myelogenous leukemia; gene expression; BAALC;
               Tanner SM,
                                                                                                          12-NOV-2002; 2002WO-US036375
                                                                                                                                            15-MAY-2003
                                                                                                                                                                          WO2003040347-A2
                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                   Brain and Acute Leukemia, Cytoplasmic alternate protein #3
                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADM46961 standard; protein; 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 145 AA;
                                             (OHIS ) UNIV OHIO STATE RES FOUND
                                                                                                                                                                                                                                                                       sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SSNGVLRÞAAÞGGIANÞEKKMNCGTQCÞNSQNLSSGÞLTQKQNGLWATEAKRDAKRMSAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVAINVTENIROMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK
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                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
               La Chapell A;
                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                        /note= "encoded by GCS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.6%;
                                                                                                                                                                                                                                                                                                                      leukemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                      prostate cancer; Brain and Acute Leukemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        649; DB 8;
No. 6.3e-65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 121;
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          WPI; 2003-441564/41.
N-PSDB; ADM46955.
                                                                                                                                                                                                                                                                                                                       acute myelogenous leukemia; gene expression; BAALC; chronic myelogenous leukemia; prostate cancer; Brai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                    Tanner SM,
                                                                                                          09-NOV-2001; 2001US-0348210P
                                                                                                                                                                  15-MAY-2003.
                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                  Brain and Acute Leukemia, Cytoplasmic alternate protein
                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADM46963 standard; protein; 149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                                                                                                      12-NOV-2002; 2002WO-US036375
                                                                                                                                                                                            WO2003040347-A2
                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                          Cytoplasmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ADM46953.
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                                                                                OHIS ) UNIV OHIO STATE RES FOUND
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                                                                                                                                                                                                                                                                              sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGIHA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAREVAINVTENIRQMDRSKRVTKNCIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GVLEDGLSSNGVLRPAAPGGIANPEKKMNCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIKAPTDSVSDEGLFSASKMAPLAVFSHGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSVLEAEKS
                                                   De La Chapell A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.0%;
67.2%;
                                                                                                                                                                                                                          "encoded by GCS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 621.5; DB 7
Pred. No. 1.1e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                          Brain and Acute Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 180;
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RESULT 11
ADQ81902
ID ADQ81902
ID ADQ81902
AC ADQ81
AC AD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
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                                                                                                                                 New polypeptide human dioxygenase 10.12 and polynucleotides encoding polypeptide, useful for treating various diseases, such as malignant tumors, inflammations, immunological diseases, hemopathy and HIV
                                                                                                                                                                                                                                                    WPI; 2002-509506/55.
N-PSDB; ADQ81901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                      Claim 1; SEQ ID NO 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-SEP-2000; 2000CN-00125495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-2000; 2000CN-00125495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human dioxygenase 10.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-SEP-2004
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                                                                                                                                                                                                                                                                                                                                                                                            (SHAN-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enzyme;
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                                                                                                                                                                                                                                                                                                                                                                                            SHANGHAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease; haemopathy; HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dioxygenase 10.12; malignant tumour; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                         BIODOOR GENE
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                                                   33pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92
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Pred. No. 6.4e
3; Mismatches
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RESULT 12
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ID ADO48
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Best Local S
           The invention relates to a novel PTH responsive gene (PAIGB) fragment encoding a polypeptide. The invention further comprises: a chimeric construct comprising the isolated nucleic acid fragment operatively linked to suitable regulatory sequences; a host cell transformed with the chimeric construct; a vector comprising the nucleic acid fragment; obtaining a nucleic acid fragment encoding the polypeptide; a method for obtaining a polypeptide detecting the presence of the nucleic acid fragment; an antibody that specifically binds to one or more epitopes of a PAIGB polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment; but that alters the expression of PAIGB gene or polypeptide; determining whether an agent alters the expression of PAIGB mRNA; determining spents for effectiveness in altering expression of the nucleic acid fragment. According to the nucleic acid fragment.
                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                           New nucleic acid fragment encoding a PAIGB polypeptide, useful preparing a composition for diagnosing, treating or preventing related disorders, e.g., osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dioxygenase 10.12, polynucleotides encoding this polypeptide, a DNA recombination process to produce the polypeptide and antagonist against the polypeptide. The present invention also discloses the method of applying the polypeptide in treating various diseases, such as malignant tumours, inflammations, immunological diseases, haemopathy and HIV infection. The present sequence is the human dioxygenase 10.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTH responsive gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse
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                                                                                                                                                                                                                                9; SEQ ID NO 10; 169pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 GPEAGGLHAGVLEDGLSSNGVLRPAAPGGTANPEKKWNCGTQCPNSQNLSSGPLTQKQNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
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                                                                                                                                                                                                                                                                                                                                                                       JA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   responsive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   osteopathic; gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein exon 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bone-forming; bone; bone density modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54
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Pred. No. 5e-29;
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                       Babij P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   splice
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expression of treating bone
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                                                                                                                                                                                                                                                                             preventing
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RESULT 13
ADM46962
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Best Local S
Matches 54
Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                                                                                                          WPI; 2003-441564/41.
N-PSDB; ADM46954.
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                                                                                                                                                                                                                                         Tanner SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-2002; 2002WO-US036375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acute myelogenous leukemia; gene expression; BAALC; chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUN-2004 (first entry)
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                                                                                                                                                                                                                                         De La Chapell A;
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100.0%; Prr
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Pred. No.
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thes 0;
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Disclosure; SEQ ID NO 20; 78pp;

English

to a BAALC alternative

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RESULT 14
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ID ADM46
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Best Local
         The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                                                                                                                                                                                        Characterizing acute or chronic myelogenous leukemia, or prostate cancer in a patient comprises assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method of characterizing acute myelogenous leukemia (AML) in a patient by assaying for the overexpression of one or more BAALC transcripts in cells obtained from the patient, where an overexpression indicates that the patient has an aggressive form of AML. The methods, kits and probes are useful for characterizing acute or chronic myelogenous leukemia, or prostate cancer. They are also useful for detecting BAALC overexpression. This sequence corresponds to a BAALC (Brain and Acute Leukemia, Cytoplasmic) protein encoded by an alternative spliced RNA consisting of exons 1, 6 and 8.
                                                                                                                                                                                       Disclosure; SEQ ID NO 18; 78pp; English.
                                                                                                                                                                                                                                                                                                                 WPI; 2003-441564/41.
                                                                                                                                                                                                                                                                                                                                                                                                                       09-NOV-2001; 2001US-0348210P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acute myelogenous leukemia; gene expression; BAALC; chronic myelogenous leukemia; prostate cancer; Brain and Acute Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brain and Acute Leukemia, Cytoplasmic alternate protein
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                                                                                                                                                                                                                                                                                                                                                    SM,
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                                                                                                                                                                                                                                                                                                                                                    De La Chapell
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Pred. No. 1.8e-24;
2; Mismatches 3
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Sequence 54

Best Query Match

Local

Similarity

36.2%;

Score 278; DB 7; Pred. No. 1.6e-23;

Length 54; Indels

Mismatches

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Gaps

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51;

Conservative

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RESULT 15
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XX Homo
XX
The invention relates to a novel PTH responsive gene (PAIGB) fragment CC encoding a polypeptide. The invention further comprises: a chimeric CC construct comprising the isolated nucleic acid fragment operatively CC linked to suitable regulatory sequences; a host cell transformed with the CC chimeric construct; a vector comprising the nucleic acid fragment; construct; a vector comprising the polypeptide; a mucleic acid fragment; construct; a vector comprising the polypeptide; a matched for cotaining a nucleic acid fragment encoding the polypeptide; a composition for regulating bone-forming activity in a mammal comprising the nucleic acid fragment, polypeptide; a composition for regulating bone-forming activity in a mammal comprising the expression of PAIGB gene or polypeptide; a creening agent alters the expression of PAIGB mRNA; cc screening agents for effectiveness in altering expression of the nucleic acid fragment; screening for agents useful for treating bone related cd disorders; a valuating the efficacy of a treatment of a bone related cd disorders; a transgenic animal comprising the DA; an animal model cor the study of bone density modulation comprising a first group of animals; studying an effect of PAIGB on bone disorders; identifying whether an agent which has bone forming activity, and a stably transfected cell line comprising two constructs, the first construct comprising a ligand binding domain which is linked to an activation domain
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                                                                            Matches
                                                                                                                  Query Match
                                                                                                                                                                                          all of which expression is driven by a constitutive promoter, the second construct comprising multiple copies of DNA binding elements linked to a minimal promoter which is linked to PAIGB cDNA, where upon the addition of chemical inducer, transcription of PAIGB gene is induced. The PAIGB polynucleotide has osteopathic activity. The PTH responsive gene may be used to treat disorders by gene thrappy. The nucleic acid is useful in preparing a composition for diagnosing, treating or preventing bone related disorders, e.g., osteoporosis. This sequence represents a PTH responsive gene protein of the invention.
                                                                                                                                                         Sequence 54 AA;
                                                                                                 Local
                                                                            51;
                    1 MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG 54
                                                                                                 Similarity
MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDAPPSAAAPDSGPEAGGLHSG
                                                                            Conservative
                                                                                               36.2%;
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Pred. No. 1.6e-23;
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Search completed: April 12, Job time: 104.667 secs 2005, 15:37:19

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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	19505, A	41874, A	57118, A	٠,	7467, Ap	3, Appli	9, Appli	27673, A	26962, A	46, Appl	11, Appl	30546, A	•	18938, A	44417, A	59848, A	2, Appli	IIIU6, A

ALIGNMENTS

RESULT 2 5198347-4 Query Match Best Local Similarity Tatches 28; Conserva RESULT 1 5198347-4 PATENT NO. 5198347 APPLICANT: Miller, LOUIS H.; ADAMS, JOHN H.; KASLOW, DAVIC C.; FANG, XIANGDOUG TITLE OF INVENTION: DNA ENCODING PLASMODIUM VIVAX AND PLASMODIUM KNOWLESI DUFFY RECEPTOR NUMBER OF SEQUENCES: 27 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/554,837 FILING DATE: 20-JUL-1990 5198347-4 5198347-4 PLASMODIUM KNOWLESI DUFFY RECEPTOR NUMBER OF SEQUENCES: 27 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/554,837 FILING DATE: 20-JUL-1990 ;SEQ ID NO:4: ; APPLICANT: Miller, LOUIS H.; ADAMS, JOHN H.; KASLOW, ;DAVIC C.; FANG, XIANGDOUG ;TITLE OF INVENTION: DNA ENCODING PLASMODIUM VIVAX AND Patent No. 5198347 SEQ ID Query Match Rest Local Similarity 31... 28; Conservative LENGTH: 778 LENGTH: 778 NO:4: 352 412 DDRSQGSLGPHTDERATLGETHMEKDTE 439 31 TDSDALPSAAATDSGPEAGGLHAGVLEDGLSSNGV-LRPAAPGGIANPEKKMNC-GTQCP 31 TDSDALPSAAATDSGPEAGGLHAGVLEDGLSSNGV-LRPAAPGGIANPEKKMNC-GTQCP 89 NSONLSS-GPLTQKQNGLWATEAKRDAK 115 TVSSDVPSVGGKDSGPSTSASHALAGENGEVHNGTDTEPKEDGEKADPQKDIEVKGKQDT Conservative 11.4%; Score 87.5; DB 31.8%; Pred. No. 0.44; tive 13; Mismatches 11.4%; Score 87.5; DB 31.8%; Pred. No. 0.44; 13; 13; Mismatches 44; 6 44; 6 Length 778; Length 778; Indels u ۲ Gaps 88

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352 TVSSDVPSVGGKDSGPSTSASHALAGENGEVHNGTDTEPKEDGEKADPQKDIEVKGKQDT

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; Sequence 2, Application US/08895590
; Patent NO. 6207410
; GENERAL INFORMATION:
   APPLICANT: Hall, Linda M.
; APPLICANT: Ren, Dejian
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Patent No. 602791
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INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 2516 amino aci
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm M.
REGISTRATION NUMBER: 39,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
OPERATING SYSTEM: FC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hall, Linda M.
APPLICANT: Ren, Dejian
APPLICANT: Zheng, Wei
APPLICANT: Dubald, Wei
TITLE OF INVENTION: Genes Encoding an Invertebrate Alphal
TITLE OF INVENTION: Calcium Channel Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 5
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699 Prince Street
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                                                                                                                                                                                                                                                                                                                                                                     10.5%; Score 80.5;
22.4%; Pred. No. 15;
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US-09-539-879A-2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2516 amino aci
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/
PILING DATE: 19-JAN-1995
PILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zheng, Wei
APPLICANT: Dubald, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 703-836-6620
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TELEPHONE: 703-C-
TO TO NO:
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REFERENCE/DOCKET NUMBER: 02:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: McGowan, Malcolm M. REGISTRATION NUMBER: 39,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 22314-3187
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                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE,
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                       308
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                                                                                                                                                                                                                                                                                                                                                                        91 QNLSSGPL-TQKQNGLWATEAKRDAKRMSAREVAINVTENIRQMDRSKRVTKNC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SSNGVLRPAAPGGIANPEKKMNC------GTQC------PNS 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
              CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                       QDLSSQTLRTAAIVAAVAAAAKEQAQEQSLADCE-SFSDRRQDADEDVRIIQDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGGGISAPPPRLTPEEAWQLQPQ------NSVTSAGSTNSSFSSGG-----GR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGSRADAIEPRY--YESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL 60
COUNTRY: USA
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                                                                 DOANE, SWECKER & MATHIS,
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Pred. No. 15;
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                                                                                                                                                                                                                                                                                                                                                                                                            307
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CURRENT APPLICATION DATA:

JTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

COMPUTER

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; ORGANISM: Human US-09-949-016-7117
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                                               SOFTWARE: FASTSEQ
SEQ ID NO 7117
LENGTH: 694
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                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                                                                                            APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                PRIOR FILING DATE:
                                                                                                                                               PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                 PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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                                                                                                                                                                                                                                                                                  FILE REFERENCE: CL001307
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/09/111,865
FILING DATE: <UNKNOWN
APPLICATION NUMBER: US 08/374,077
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:

NAME: NCGOWAN, MALCOLM M.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 022650-264
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-6620
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5. 6812339
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39; Conserv
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                                                                                            for Windows Version 4.0
                                                                                                                                                                   2000-10-03
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22.4%; Pro
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Pred. No. 15;
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                                                                                                                               SEQ ID NO 1
LENGTH: 724
TYPE: PRT
Query Match
Best Local Similarity 27...
Thes 31; Conservative
                                                                                                                                                                                              Sequence 1, Application US/09121964
Patent No. 6124447
GENERAL INFORMATION:
APPLICANT: Natori, Shunji
TITLE OF INVENTION: NOVEL ENZYME CATALYZING DEPHOSPHORYLATION
FILE REFERENCE: 32290-144753
CURRENT APPLICATION NUMBER: US/09/121,964
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 9
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SEQ ID NO 18465
LENGTH: 244
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                             ORGANISM: Sarcophaga peregrina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                    192 CRLASGSTSKTSTSVASSGVSKPRWRKRRRQTSARLT--IRQARRT-GTSKPAIN 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 GAPLRING--RPSASSGIASPSAIPHCARPQAAHQRQRPRRPANSQSSRATARNDSQNPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 ALGPKASPAPSHNSGTPAPYAQAVAPPAPSGPST 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 TDSEVSOSPAKNGSKPVHSNOHPOSPAVPPTYPSGPPPAASALSTTPGNNGVPAPAAPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 -- LSSGPLTQKQNGLWATEAKRDAKRMSAREVAINVTENIRQMDRSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 EDGLSSNGVLRPAAPGGIANPEKKMNC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 GCQASARPASRPSARNSRSSETPAARSSPSPSPGTHSSRLPARAGGTTSSSIQGTASRLA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 -- GGIANPEKKMNCGTQCPNSQNLS----SGPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 TDSDALPSAAATDSGPEAGGLH------AGVLEDGLSSNGVLRPAAP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GCGGSRADAIEPRYYESWTRETESTWLT-----YTDSDALPSAAATDSGPEAGGLHAGVL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
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ON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
ON: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1998-02-18
UMBER: US 60/094,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1998-07-27
                        10.2%; Score 78; DB 27.7%; Pred. No. 4.9; ive 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.3%; Score 79; DB 24.0%; Pred. No. 0.76 tive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 79.5;
Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.78;
                                                         DB 3; Length 724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 244;
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                         39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 694;
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                         34;
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                         Gaps
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RESULT 10
US-09-071-035-176
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US-09-252-991A-32740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-32740
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SEQ ID NO 32740
LENGTH: 715
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 176, Application US/09071035
Patent No. 6448043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Marc J. I
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32740, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE:
CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                   APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                     COUNTRY: U
                                                                                                                                                                                                                CITY: Rockville
                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417 AAARKSAVQLQGMHAGDAENGIHAVVGQQADQGLAGGEGLLWLHGQYPHPVRRPSESPFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 -----RPAAPGGIANPEKKWNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 AAATDSGPEAGGLHAGVLEDGL-----SSNGVL-----
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Similarity 17.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A-----KRMSAREVAINVTEN-----IRQMDRSKRVTKNCI 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PQRSCSHSHKREGEPSCPPGLQPLASRINAST-----ASAPSASASNGLTSSSSKRS 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marc J. Rubenfield et al.

NVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

NVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                          Maryland
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                                                                                                                                                                                                                                    E: Human Genome Sciences,
9410 Key West Avenue
                                                                                                                                                                         USA
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US/09/071,035
                                                                                                     3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-071-035-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 174, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
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TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 174:
SEQUENCE CHARACTERISTICS:
                                                                        ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: HP Vectra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gil H. CI
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: STRANDEDNESS: BILL
                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MSDOS version 6.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 27.1 les 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 LTAATTSQADQNNFRVLYYAEKEAIPVNDARVNQLTPISSFEKKTYGSDAEAKNAVN 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 W--ATEAKRDAKRMS----AREVAINVTE-NIRQMD-----RSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50
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                                                                                                                                                                                                                                                                                                                                                                                                                    20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rockville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGGKSTENTDSRSSAAESTTVESTKASATKESSSK-ATTKSSDAKPSGTTTADSKATAS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                     E: Diskette, 3.5
HP Vectra 486/33
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                                                                                                                                                                                                                                                                            US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                       3.50 inch, 1.4Mb
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Pred. No. 2.5;
16; Mismatches
                                                                                                     PB369P2
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RESULT 13
US-09-328-352-8115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09408647A Patent No. 6399858 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: Rut-Cook 98-0090
CURRENT APPLICATION NUMBER: US/09/408,647A
CURRENT FILING DATE: 1999-08-26
PRIOR APPLICATION NUMBER: 60/098,036
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (196)...(290)
NAME/KEY: DOMAIN
LOCATION: (30)...(483)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank No. 6399858 AF014950
DATABASE ENTRY DATE: 1997-09-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SIGNAL
LOCATION: (1)...(41)
NAME/KEY: DOMAIN
LOCATION: (196)...(29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kobayashi, Donald
TITLE OF INVENTION: Chitinase Gene from Stenotrophomonas
TITLE OF INVENTION: maltophilia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Stenotrophomonas
                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: 11
                                                                                   279
                                                                                                                                                                                                                                                      159
                                                                                                                        119 AREVAINUT 127
                                                                                                                                                                  219 LVWSAATDNSGGSGVAGYDVYRNGSLVGSPSATQYTDGGLTASTAYTYTVRARDNAGNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 LTAATTSQADQNNFRVLYYAEKEAIPVNDARVNQLTPISSFEKKTYGSDAEAKNAVN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 W--ATEAKRDAKRMS----AREVAINVTE-NIROMD------RSKRVTKNCIN 145
                                                                                                                                                                                                                                                                                           26 TWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGLSSNGVLRPAAPGGIANPEKKM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                          -----NCG-----TQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STKEA-----ANNGSAEKQSPAKNANPDDQANQVLNQLANMFPGQGLPQAILTSQTNNF 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLHAGVLEDGLSSNGVLRPAAPGGIANPEKKMN-CGTQCPN---SQNLSSGPLTQKQNGL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGGKSTENTDSRSSAAESTTVESTKASATKESSSK-ATTKSSDAKPSGTTTADSKATAS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGG-----SRADAIEPRYYESW----TRETESTWLTYTDSDALPSAAAT-DSGPEAG 49
                                                                                 AQSGSİSVT 287
                                                                                                                                                                                                                                                      TWANASAGSHTFKAVATDNNNAVTSSATVSVTVTASSNDTTPPSVPGGLASPSKTATTVN 218
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22.5%;
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                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                          DB 3;
                                                                                                                                                                                                                                                                                                                                     58; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                            Length 700;
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US-09-618-425-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gry L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09618425
Patent No. 6475744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8115, Application US/09328352 Patent No. 6562958
                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 00786-428001
CURRENT APPLICATION NUMBER: US/09/618,425
CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/203,005
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 60/145,363
PRIOR FILING DATE: 1999-07-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Shearman, Lauren
TITLE OF INVENTION: METHODS FOR IDENTIFYING COMPOUNDS
TITLE OF INVENTION: MODULATE CIRCADIAN RHYTHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Reppert, Steven M.
APPLICANT: Weaver, David R.
APPLICANT: Zylka, Mark
APPLICANT: Jin, Xiaowei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
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                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1113
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                                      107 ATEAKRDAKRMSAREVAINVTEN-IRQMDRSK 137
                                                                             914 QLNLLQEEMPAPSESADAVRRG-AGPDAKHHCVTGPSGSRSRHCTSGELATATAHQESAA
                                                                                                                                                       860 LGAAGSSELAPLVPAMAPNPEPTTSGHSQRRVEENWEAH--SEELPFISSRSSSP----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 ----GPQASGDPRSAAP 244
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                                                                                                                52 HAGVLEDGLSSNGVLRPAAPGGIANPEKKWNC--GTQCPNSQNLSSGPL---TQKQNGLW 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 VLEDGLSSNGVLRPAAP 71
                                                                                                                                                                                              1 MGCGGS-----RADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGL
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                                                                                                                                                                                                                                                         Similarity
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Similarity 33.8%;
ASGSSASSIYFSSTDYASEVSENRQRPQDRQR 1004
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                                                                                                                                                                                                                                                     Score 74;
Pred. No.
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Pred. No. 14;
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Sequence 723, Application US/09538092

| Sequence 723, Application US/09538092
| Patent No. 6753314
| GENERAL INFORMATION:
| APPLICANT: Giot, Loic
| APPLICANT: Giot, Loic
| APPLICANT: Wansfield, Traci A.
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
| FILLE REFERENCE: 15966-542
| CURRENT APPLICATION NUMBER: US/09/538,092
| CURRENT FILING DATE: 2000-03-29
| PRIOR APPLICATION NUMBER: 60/127,352
| PRIOR APPLICATION NUMBER: 60/178,965
| PRIOR APPLICATION NUMBER: 60/178,965
| PRIOR APPLICATION NUMBER: 60/178,965
| PRIOR APPLICATION SIMPLE: 2000-02-01
| NUMBER OF SEQ ID NOS: 1387
| SOFTWARE: CURAPATS EQUO-02-01
| SEQ ID NO 723
| LENGTH: 346
| TYPE: PRT ORGANISM: Saccharomyces cerevisiae
| FEATURE: NAME/KEY: misc feature
| LOCATION: (0). . (0)
| OTHER INFORMATION: Polypeptide Accession Number YOR007C
| US-09-538-092-723
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Search completed: April 12, 2005, 15:43:30 Job time : 27.6667 secs
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US-09-538-092-723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.6%; Score 73.5; DB 4; Length 346; Best Local Similarity 29.4%; Pred. No. 5.6; Matches 37; Conservative 11; Mismatches 51; Indels 2.
                                                                                                               320 LRNMAG 325
                                                                                                                                                                                                                           261 -GĞLMINIPQLMQAAQKIMISNIPĞAMQNIQKIMIQDPSIRQMAEGFASĞGGTPNLSDLMINIPA 319
                                                                                                                                                                                                                                                                                                                                       201 GDNATEAMKRDYESAKKKVEQSLNLEKTVPEQSRDADVDASQGASAGGLPDLGSLLGGGL 260
                                                                                                                                                                   99 TOKONG 104
                                                                                                                                                                                                                                                                            57 EDGLSSNGVLRPAA-----PGGIANPEKKMN------CGTQCPNSQNLSSGPL 98
                                                                                                                                                                                                                                                                                                                                                                                        5 GSRADAIEPRYYESWTRETE-STWLTYT-----DSDALPSAAATDSG-PEAGGLHAGVL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                27; Gaps
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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          649
472:5
472:5
2788
2778
140
99
86
84
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

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13: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US10RW_PUB.pep:*

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36.2
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Copyright (c) 1993 - 2005 Compugen Ltd.
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14 US-10-293-239-19

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14 US-10-293-239-21

14 US-10-293-239-18

14 US-10-293-239-37

15 US-10-293-239-37

16 US-10-293-239-37

17 US-10-293-239-35

18 US-10-293-239-35

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Sequence 17, Appl
Sequence 30, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 20, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 35, Appl
Sequence 48905, A
Sequence 60, Appl
Sequence 60, Appl
Sequence 112, App
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82		4 5 C S	15	-10-43/-963-14498 -10-424-599-19365	Sequence 144983,
82		1479	16	-10-437-963-18021	
81		219	14	-10-156-761-1344	equenc
80.5		600	16	-10-408-765A-194	equence 1945, A
		528	16	-10-437-963-1736	equence 173618
80		1108	10	-09-949-029-108	
79.5		996	16	S-10-437-963	e 114095,
79		876	9	09-801-368-44	_
78.5		1274	16	-10-437-963-18022	
78		1491	16	-10-437-963-14019	10
77.5		670	14	-10-156-761-141	Sequence 14107, A
77		268	15	-10-369-493-824	Sequence 8240, Ap
•		320	15	-10-425-114-433	Sequence 43318, A
•	•	426	15	-10-369-493-392	Sequence 3926, Ap
J		391	16	-10-437-963-17790	Sequence 177907,
•		276	16	0-437-963-15827	Sequence 158275,
•		286	9	-071-035-17	Sequence 176, App
•		286	14	0-206-576-17	Seguence 176, App
		286	17	0-912-362-17	Seguence 176, App
•		305	9	-071-	Sequence 174, App
•		305	14	-10-206	Sequence 174, App
•		305	17	-10-912	174
•	•	373	16	-10-437	104
75		167	16	-10-767	Seguence 46805, A
75		604	16	-10-437	æ
4.		296	16	-10-437	e 19369
4		580	15	-10-282	73164,
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4.		601	15	-10-282	
74	9.6	332	16	-10-437	w
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ALIGNMENTS

US-10-293-239-17

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; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-239-17
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Publication No. US20030119043A1
GENERAL INFORMATION:
APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
                                                                                                                                                                                                                                                                                Query Match 84.6%; Score 649; DB 14; Length 145; Best Local Similarity 83.4%; Pred. No. 8.6e-60; Matches 121; Conservative 10; Mismatches 14; Indels
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CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
61 PSNGVPRSTAPGGIPNPEKKTNCETQCPNPQSLSSGPLTQKQNGLQTTEAKRDAKRMPAK
                                                                                                                        61 SSNGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAR 120
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-239-19
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Sequence 19, Application US/10293239
Publication No. US20030119043A1
GENERAL INFORMATION:
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APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
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Publication No. US20030143743A1
GENERAL INFORMATION:
APPLICANT: Schuler, Gerold
APPLICANT: N.V. Antwerps Innovatiecentrum
TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
TITLE OF INVENTION: Polymucleotides by Electroporation
FILE REFERENCE: 021505wo/JH/ml
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 145
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Best Local Similarity 83.49
Matches 121; Conservative
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                                         61 KIKAPTDSVSDEGLFSASKMAPLAVFSHGMLEDGLPSNGVPRSTAPGGIPNPEKKTNCET 120
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  QCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAREVAINVTENIRQMDRSKRVTKNCIN 145
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                                                                                                                                                                                                                               81.0%; Score 621.5; DB 1
67.2%; Pred. No. 8.6e-57;
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83.4%; Pred. No. 8.6e-60;
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APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 149
TYPDE: DRT
                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 73
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Best Local :
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APPLICANT: de la Chapelle, Albert
ITILE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR PILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
NUMBER OF SEQ ID NOS: 39
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                                                                                              Similarity
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Similarity 65.3%;
                       MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLED 58
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                                                                          Conservative
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                                                                                            37.5%;
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                                                                        Score 288; DB 14;
Pred. No. 2.2e-22;
2; Mismatches 3;
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RESULT 6

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US-10-293-239-18
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 80
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Publication No. US20030119043A1
GENERAL INFORMATION:
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Best Local Similarity
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Publication No.
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Best Local Similarity 94.4%;
Matches 51; Conservative
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SEQ ID NO 18
LENGTH: 54
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APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
PRIOR FILING DATE: 2001-11-09
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APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
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APPLICANT: de la Chapelle, Albert
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No. US20030119043A1
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94.3%;
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Pred. No. 1.
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Pred. No. 1.7e-21;
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NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 35
LENGTH: 18
                                                                    NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 180225
LENGTH: 1597
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Publication No. US20030119043A1
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SEQ ID NO 37
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Best Local Similarity
                                                                                                                       APPLICANT: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53221) B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/293,239
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/348,210
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                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tanner, Stephan
APPLICANT: de la Chapelle, Albert
TITLE OF INVENTION: BAALC expression as a diagnostic marker for acute leukemia
FILE REFERENCE: 22727/04101
                                                                                                                                                                                                                              APPLICANT:
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OTHER INFORMATION: Clone ID: PAT_MRT4530_77610C.1.pep
                       FEATURE:
                                                      TYPE: PRT
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ORGANISM: Homo sapiens
                                  ORGANISM: Oryza sativa
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Zhou, Yihua
Cao
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Wei
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100.0%; Pred. No.
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; Pred. No. 1.8e-07
0; Mismatches 0
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APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Se
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: LIB3476-020-P1-K1-A12.pep US-10-767-701-48905
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Publication No. US20040172684A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 48905
LENGTH: 147
Type. Der
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APPLICANT: Busby, R
APPLICANT: Cali, B
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APPLICANT:
APPLICANT:
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APPLICANT:
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Best Local :
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                                                                                                                                                                                                                                                                                                   Hecht, Peter
Holtzman, Doug
Madden, Kevin
                                                                                                                                                                                                   Royer, John
Salama, Sofie
                                                                                                                                                                                                                                                              Maxon, Mary
Milne, Todd
                                                                                                                                                                                                                                                                                                 Madden,
                                                                                                                                                                                                                                          No. US20020128250Alman,
                                                                                                                                                                                                                                                                                                                                                              Cali, Brian
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Pred. No.
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                                                                                                                          Secondary Metabolite Production in Fungi
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US-10-149-310-112
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                                                                                                                                       Sequence 65588, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.1 SEQ ID NO 112
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/149,310
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: PCT/US01/29288
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: US 60/233,564
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 308
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Best Local Similarity
                                                                                                APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
                      APPLICANT:
                                                              APPLICANT:
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NUMBER OF SEQ ID NOS: 440
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Modulation of Secondary Metabolite Production TITLE OF INVENTION: Zinc Binuclear Cluster Proteins FILE REFERENCE: 14184-019US1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1433
TYPE: PRT
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                                                        Zhou, Yihua
Kovalic, David K.
Screen, Steven B
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Madden, Kevin T.
Maxon, Mary
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APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 144983
ILENGTH. 600
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US-10-425-114-65588
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US-10-437-963-144983
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                                                                                                                                                                                                                                                                           Query Match 10.8%; Score 82.5; DB 16; Length 609; Best Local Similarity 25.7%; Pred. No. 11; Matches 38; Conservative 21; Mismatches 68; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 144983, Application US/10437963 Publication No. US20040123343A1
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Best Local S
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
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ORGANISM: Oryza sativa
PEATURE:
NAME/KEY: unsure
LOCATION: (1)..(609)
OTHER INFORMATION: unsure at all Xaa locations
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                                              109 EAKRDAKRMSAREVAINVTENIRQMDRS 136
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  138 NSVTTAIRDSIRETAIGKTRNTEKADRA 165
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                                                                                                                                 52 HAGVLEDGLSSNGVLRPAAPGGI-ANPEKKMNCGTQCPNSQNLSSGPLTQKQN--GLWAT 108
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Post-processing: Minimum Match 0%
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RESULT 2 GNVSSC genome polyprotein - sug: yenome polyprotein - sug: yenome polyprotein - sug: C;Date: 30-Jun-1993 #seq C;Date: 30-Jun-1993 #seq C;Accession: PH0207 R;Frenkel, M.J.; Jilka, U.J. J. Gen. Virol. 72, 237-2. A;Title: Unexpected sequence number: PH0207 A;Reference number: PH0207 A;Recession: PH0207 A;Recession: PH0207 A;Residues: 1-365 <fre>A;Cression: CFRE>A;Cross references: UNIPIC;Superfamily: tobacco et c;Keywords: coat protein. F;1-52/Product: nuclear: F;53-365/Product: coat pl</fre>	RESULT 1 A35970 erythrocyte-binding protein - C;Species: Plasmodium knowles C;Date: 14-Dec-1990 #sequence C;Accession: A35970 R;Adams, J.H.; Hudson, D.E.; Cell 63, 141-153, 1990 A;Title: The duffy receptor f A;Reference number: A35970; M A;Accession: A35970 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-778 <ada> A;Cross-references: UNIPROT:P C;Keywords: transmembrane pro C;Keywords: transmembrane pro Query Match Best Local Similarity 31. Matches 28; Conservative Oy 31 TDSDALPSAANTDSG OY 89 NSQNLSS-GPLTOKO ON 11 </ada>	\$4444000000000000000000000000000000000
WSSC contains: carboxyl end partial partial partial product: pH0207 p	ocyte-bindi: ies: Plasmo: 11-Dec-19 sion: 14-Dec-19 sion: A359 sio	70.5 70.5 70.5 70.5 70.5 70.5 70.5 70.5
/protein - sugarcane mosa carboxyl end of nuclear sugarcane mosaic virus, -Jun-193 #sequence_revis n: PH0207 M.J.; Jilka, J.M.; McKer rol. 72, 237-242, 1991 nexpected sequence divers number: PH0207; MUID:91 nexpected sequence rNA pH0207; PH0207; VIII supper: Genomic RNA 1-365 <fres ferences: UNIPROT:P25242; lly: tobacco etch virus g coat protein; inclusion duct: nuclear inclusion product: coat protein #sta</fres 	plasmodium knowlesi Dec-1990 #sequence_revis Dec-1990 #sequence_revis L: A35970 1-153, 1990 1-153, 1990 1-153, 1990 1-153, 1990 1-153, 1990 1-178 <ada> reliminary type: DNA 1-778 <ada> erences: UNIPROT:P22545; erences: UNIPROT:P22545; 1 Similarity 31.8%; P 28; Conservative 13; 31 TDSDALPSAATDSGPEAGGL 52 TVSSDVPSVGGKDSGPSTSAS 89 NSQNLSS-GPLTQKQNGLMAT : : 12 DDRSQGSLGPHTDERATLGET</ada></ada>	
sugarcane mosai end of nuclear mosaic virus, s sequence_revis a, J.M.; McKerr 7-242, 1991 equence divers H0207; MUID: 911 mic RNA B:	wlesi wlesi ence_rev E.; Tori cor famil 0; MUID: 07:P2254 ; protein 11.4%; 31.8%; 31.8%; itive 1 itive 1 iTDSGPEAG iTDSGPSTS ;KDSGPSTS	351 542 1343 1343 3623 3623 3623 3623 367 500 500 500 367
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SC) (fragment) In b; coat protein P.M.; Clark Jr., J.M.; Shukla, D.D. terminal ends of the coat proteins (1866 1222123; PIDN:BAA00796.1; PID:g22212	Htext_change 09-Jul-2004 Wellems, T.E.; Aikawa, M.; Miller, I where is located within the microne. 17513; NID:g160273; PID:g160274 Length 778; Length 778; Landels 3; Gaps 3; LPAAPGGIANPEKKMNC-GTOCP 88	helix-loop-helix t sulface-binding pr gag polyprotein - probable sugar ABC cell division prot probable TMV resis intrinsic factor-B transforming prote pregnancy-specific hypothetical prote t-complex protein hypothetical prote 3-dehydroquinate s transcription fact phage-related inte Ig mu chain C regi

Query Match Best Local Similarity

11.0%; 21.6%;

Score 84; DB 1; Pred. No. 2.7;

Length 365;

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N;Alternate names: MSP8 protein; protein YM8021.06.
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence revision 01-Sep-1995
C;Accession: S54587; S48234; S61595; S49498
R;Pearson, D; Bowman, S.
submitted to the EMBL Data Library, May 1995
A;Accession: S54587
A;Accession: S54587
A;Accession: S54587
A;Accession: S4588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: S
A;Map position: 13R
C;Superfamily: GAL4 z
C;Keywords: transmemb
    RESULT 4
T43456
hypothetical protein DKFZp434L061.1 -
hypothetical protein (man)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-302, 'A',304-767,'A',769-998,1003-1007,'S',1009-1015,'Q',1017-1018,'P',1020
A;Residues: EMBL:X94215; NID:g1122900; PIDN:CAA63906.1; PID:e214033; PID:g112290
A;Experimental source: strain ENY.WA-1A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Grzesitza, D.
submitted to the EMBL Data Library, March
A;Reference number: S48234
A;Accession: S48234
A;Molecule type: DNA
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A; Residues: 1-746; 'L', 748-1433 < GRZ>
A; Cross-references: EMBL: X78344; NID: g559523; PIDN: CAA55139.1;
R; Boles, E.; Hettmann, C.; Zimmermann, F.K.
submitted to the EMBL Data Library, December 1995
A; Reference number: S61594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: SGD:CAT8; MSP8
A;Cross-references: SGD:S0004893; MIPS:YMR280c
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A;Cross-references: UNIPROT:P39113;
A;Experimental source: strain AB972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Keywords: transmembrane protein
;65-102/Domain: GAL4 zinc binuclear cluster homology <GAL4>
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 32; Conserv
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                                                                                                                                                                                                                                                                                                    LPSAAATDSGPEAGGLHAGVLEDGLSSNGVLRPAAPGGIANPEKKMNCGTQCPNSQNLSS
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                                                                                                                                                                     GHSPMINITNGNKRLKYEKDAKR-NAKDGGISKGENAHNFONDIKKNMS
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#sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
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90
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                                                                                              RESULT 6
A57988
  regulatory protein areA - Emericella nidulans (;Speciaes: Emericella nidulans, Aspergillus nidulans (;Speciaes: Emericella nidulans, Aspergillus nidulans C;Date: 26-Jul-1996 #sequence revision 26-Jul-1996 #text_change C;Accession: A57988; S10017; S70168; S72883
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R;Poustka, A.; Klein, M.; Me
submitted to the Protein Seq
A;Reference number: Z22516
A;Accession: T43456
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Bahri, S.M.; Yang, X.Y.; Chia, W.

Mol. Cell. Biol. 17, 5521-5529
Mol. Cell. Bros. 17, 5521-5529
A;Title: The Drosophila bifocal gene encodes a novel protein which A;Reference number: Z15048; MUID:97415628; PMID:9271427
A;Accession: T03743
                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: FlyBase: FBgn0014133
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:O16125; EMBL:AF011791; NID:g2388667; PIDN:AAB69991.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
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C; Superfamily: hydroxyproline-rich glycoprotein
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A;Residues: 1-571 <AAA>
A;Cross-references: UNIPROT:075175; EMBL:AL133647
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CSKTKSIS
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                                                                                                                                                                                                                                                                                                                 Conservative
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Pred. No. 2
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Pred. No. 12
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09-Jul-2004

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A;Introns: 147/2
C;Function:
A;Description: med
C;Superfamily: nit
C;Keywords: DNA b:
F;670-723/Domain:
F;673-697/Region:
C;Accession: C69899
C;Accession: C69899
C;Accession: C69899
C;Accession: C69899
C; Ston, S; Brouillet, S; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho C; Bron, S; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho C; Bron, S; Bruillet, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, C.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.;
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A;Title: Mutational analysis reveals dispensability of the N-terminal region o A;Reference number: S70167; MUID:96123430; PMID:8596437
A;Accession: S70168
                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein yobL - Bacillus subtilis C;Species: Bacillus subtilis C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #tex
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A; Residues: 158-876 < KU2>
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A; Residues: 1-876 < CAD>
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A; Residues: 1-791, 'A', 793, 'T', 795, 'SPGTNS', 802-876
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A; Residues: 1-876 < KUD>
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Title: The regulatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    645
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$72883
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                        elongation factor EF-2 [imported] - Guillardia theta nucleomorph C;Species: nucleomorph Guillardia theta  
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C;Accession: G90128  
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Nature 410, 1091-1096, 2001  
A;Title: The highly reduced genome of an enslaved algal nucleus. A;Reference number: A99082; MUID:11323671; PMID:11323671
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C;Accession: T37073
R;Sanders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, submitted to the EMBL Data Library, August 1999
A;Reference number: Z21621
A;Accession: T37073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Title: The complete genome sequence of the Gram-positive bacterium A;Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-269 <SAN>
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A;Experimental source: strain 168
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A; Residues: 1-600 < KUN>
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A;Experimental source: strain A3(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Streptomyces coelicolor; Date: 03-Dec-1999 #sequence_revision
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                                                                                 11 IEPRYYESWT-----RETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGL
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                                           LPPTHVEQWVPVNFHCRPRRRVLRSGGLTFSPTTVLPSRGCCGSGERTGG.
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Pred. No. 16;
22; Mismatches
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Pred. No.
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probable guanine nucleotide exchange fact N;Alternate names: Shar pei/DRhoGEF2 C;Species: Drosophila melanogaster C;Date: 11-Jun-1999 #sequence revision 11 C;Accession: T09144; T09223 R;Haecker, U; Perrimon, N. submitted to the EMBL Data Library, Octob A;Reference number: Z16586
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A;Map position: 2; 53F1-2
A;Note: orchantur
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                                                                                                                                                                                                    A;Description: mediates actin rearrangements required for cell shap C;Superfamily: rat Munc13-3 protein; protein kinase C zinc-binding C;Keywords: embryo; GTP exchange; signal transduction F;1151-1200/Domain: protein kinase C zinc-binding repeat homology <
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A;Residues: 1-2559 <HAE>
A;Cross-references: UNIPROT:O44113; EMBL:AF031930; NID:g2687355; P
A;Cross-references: UNIPROT:O44113; EMBL:AF031930; NID:g2687355; P
R;Barrett, K.; Leptin, M.; Settleman, J.
Cell 91, 905-915, 1997
Cell 91, 905-915, 1997
A;Title: The Rho GTPase and a putative RhoGEF mediate a signaling
A;Reference number: Z16618; MUID:98088790; PMID:9428514
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A; Genome: nucleomorph
C; Superfamily: translat:
C; Keywords: nucleomorph
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Best Local Similarity
Matches 28; Conserv
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                              VLRPAAPGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSARE 121
                                                                  GSSPDNMHPRHPDRITKTTSGSW-EIVEKDGESSPPGTPPPPYLSSSHMTVLEDPNENNR 857
GAAAAGPGVFIESHQ---
                                                                                                     GSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAGVLEDGLSSNG
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                                                                                                                                       Conservative
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Pred. No. 1.
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 -FTPMAGASSPIPISLHSNHMHAAQSNDTQKEIISME
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                                                                                                                                      Mismatches
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l.1e+02;
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serotonin receptor 2B - fruit fly (Drosophila melanogaster)
N/Alternate names: 5-hydroxytryptamine receptor 2B (5-HTR2B)
C;Species: Drosophila melanogaster
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
C;Accession: S19156; S18154
D.Candon
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S19156
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JE0301
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                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-516 <OHT>
A; Cross-references: UNIPROT:074641; UNIPROT:08X217;
C; Superfamily: Penicillium purporogenun inulinase
C; Keywords: glycosidase; hydrolase
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A;Map position: 3
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A; Residues: 1-781 < WOO>
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;Acc;Saudou, ...
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Best Local 8
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     F.; Boschert,
1, 7-17, 1992
                                                                                                                                                                                         413 SEQTVINYTQSNATLSVDRTESGDISYDPAAGGVHTAKLEEDGTGLVSIRVL 464
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                                                                                                                                                                                                                                                         Score 76; DB Pred. No. 23; 6; Mismatches
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Pred. No.
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5; Mismatches
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                      Plassat,
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                        J.L.; Hen,
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RESULT 14
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Nature 413, 848-852, 2001
Nature 413, Earry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable transport system periplasmic binding protein STY2452 [imported] - Salmonella C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AH0784 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churche R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Dowd, L.; White, N.; Farra C., Conto, R.; Conto, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra C., Conto, R.; Conto, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra C., Conto, R.; Conto, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra C., Conto, R.; Conto, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra C., Conto, R.; Conto, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra C., Conto, R.; Conto, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra C., Conto, R.; Conto, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra C., Conto, R.; Conto, R.; Conto, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra C., Conto, R.; 
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A; Residues: 1-601 < PAR>
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C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F;124-145/Domain: transmembrane #status predicted <TM1>
F;156-177/Domain: transmembrane #status predicted <TM2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Statue: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :597-619/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;284-305/Domain: transmembrane
;564-587/Domain: transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Gene: FlyBase:5-HT1B
;Cross-references: FlyBase:FBgn0004572
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: GB:AL513382; PIDN:CAD02598.1; PID:g16503454; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                              396
                                                                                                                                                                                                                                                                                    342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                489
452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85
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                                                                                                                                                                                                                                                                                                                                                        15 YYESWTR-----ETESTWLTYTDSDA-----LPSAAATD--SGPEAGGLHAGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-645 <SAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                   DAKRMSAREVAINVTENIROMDRSK 137
                                                                                                                                          -DGYDRENLLKADALLTQAGWVINGQQRVNSVTGKPLTFELL---LPASSNSQWVLPFQH
                                                                                                                                                                                                             EDGLSSNGVLRPAA----PGGIANPEKKMNCGTQCPNSQNLSSGPLTQKQNGLWATEAKR 112
                                                                                                                                                                                                                                                                                    FYNAWSRTNSYFQNTEYAARNYPDADELVLLAPMKKDLPPEVFTQIYQPPVSNG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYTDSDALPSAAATDSGPEAGGLHAGVLEDGLSSNGVLRPAAPGG----IANPEKKMNCG
   NLQR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOCPNSQNLSSGPLTQKQNGLWATEAKRDAKRMSAREVAI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTPSEKALSGAGTVAGAVAGGSGSGSGSGEGAGTEGKNAGVGLGGVLASTANPHQKL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     periplasmic oligopeptide-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
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ilarity 22.8%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.9%;
llarity 31.0%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNIPROT: P28286; EMBL: Z11490; NID: g7506; PIDN: CAA77571.1; PID: g7507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----AKRRQL--LEAKRE--RKAAQTLAI
-LGITMTIRQVDNSQ 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 74.5;
Pred. No. 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
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Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher.
Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 601;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
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RESULT 15

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period protein Per3 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14260
R;Zylka, M.J.; Shearman, L.P.; Weaver, D.R.; Reppert, S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuron 20, 1103-1110, 1998
A;Title: Three period homologs in mammals: differential light
A;Reference number: Z17943; MUID:98318231; PMID:9655499
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C;Keywords: circadian rhythm
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1113 <ZYL>
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                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross_references: UNIPROT:070361; EMBL:AF050182; NID:g3136149; PID:g3136150; PIDN:AAC4
                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 38
                                         107 ATEAKRDAKRMSAREVAINVTEN-IROMDRSK 137
                                                                                     914 QLNLLQEEMPAPSESADAVRRG-AGPDAKHHCVTGPSGSRSRHCTSGELATATAHQESAA 972
                                                                                                                                                                          860 LGAAGSSELAPLVPAMAPNPEPTTSGHSQRRVEENWEAH--SEELPFISSRSSSP----L
                                                                                                                              52 HAGVLEDGLSSNGVLRPAAPGGIANPEKKNNC--GTQCPNSQNLSSGPL---TQKQNGLW 106
                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                      1 MGCGGS-----RADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGL
                                                                                                                                                                                                                                                                                         Similarity
ASGSSASSIYFSSTDYASEVSENRORPODROR 1004
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                      9.6%; Score 74;
25.0%; Pred. No.
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                                                                                                                                                                                                                                                             70;
                                                                                                                                                                                                                                                                                                              Length 1113;
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                                                                                                                                                                               913
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Search completed: April 12, 2005, 15:44:46 Job time : 22.6667 secs This Page Blank (uspto)

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Maximum Match 100%
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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Perfect score:
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                  649
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Gapop 10.0 ,
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(without alignments)
784.347 Million cell updates/sec
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10.1101/gr.1451 gahara Y., Shib ashizaki Y., rapper-selected	roup Phase I & sed on function	i0.1038/35055500; mouse cDNA collection.	:10.1016/S0076-6 .ng.";	0.1073/pnas.2 L.J., Plass J.E., Archer Mapelle A.; Walian neuroecand acute levas	Vertebrata; I	e update) ion update) s neonate ce: e:9630028H16	5 AA.	TS	•
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RC STRAIN=C55BL/6J; TISSUE=Cerebellum;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA KOnno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,

RA Konno H., Shii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RICEN integrated sequence analysis (RISA) system-384-format

Sequencing pipeline with 384 multicapillary sequencer.";

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Matches 145
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01-DEC-2001
01-DEC-2001
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01-DEC-2001 (TrEMBLrel. 19, Last sequence up
05-JUL-2004 (TrEMBLrel. 27, Last annotation
Dem-A20-4 (BAALC isoform 1-6-8).
Name=dem-A20-4; Synonyms=Baalc;
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                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
     SEQUENCE FROM N.A
                                                      SEQUENCE FROM N.A. Wang X., Tian Q.,
                                                                                                                                                                                                                                                                                       Q920K5
                                                                                                        NCBI_TaxID=10116;
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Genome Res. 10:1617-1630(2000).
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RC TISSUE-Whole embryo;
RC PubMed=14702039, DOI=10.1038/ng1285;
RC PubMed=14702039, DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
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RA Yamamoto J., Saito K., Kakami R., Kandi R., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Sudo H., Kamata K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Ninomiya K., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Moriya S., Momiyama H., Ishima A., Sasaki N., Aotsuka S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
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RA Hishigaki H., Watanabe K., Kumagai A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Takemoto M., Kawakami B.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Matsumura K., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Motiyani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Motiyani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
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Q9HA93;
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Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 28, Last annotation update)
Q1-Created protein FLJ12015 (BAALC isoform 1-6-8)
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Mammalia; Eutheria;
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altcchul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

A Altcchul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Richards S., Worley N.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Richards M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,

RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

A Macywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

RA Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Strausberg R.;

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ day

EMBL; AK022077; BAB13960.1; -.

REMBL; AF37313; AAL50515.1; -.

REMBL; BC011517; AAH15157.1; -.

REMBL; AF363578; AAL50377.1; -.

REMBL; AF363578; BAALC N.;

InterPro; IPR009728; BAALC N.;

Pfam; PF06989; BAALC N; 1.

REOUENCE 145 AA; I5551 MW; CFB92BBE283DD92E
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Best Local S
Matches 121
   Q8WNE9;
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Nakai K.,
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TISSUE-Brain;
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"BAALC, the human member of a novel mammalian neuroectoderm general plineage, is implicated in hematopoiesis and acute leukemia.";

Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
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Proc. Natl. Acad. Sci. U.S.A. 5
EMBL; AF371322; AAL50518.1; -.
Pfam; PF06989; BAALC N; 1.
Pfam; PF06989; BAALC N; 1.
145 AA; 15401 MW;
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE=2157484; PubMed=11707601; DOI=10.1073/pnas.241525498;

MEDLINE=2157484; PubMed=11707601; DOI=10.1073/pnas.241525498;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen Mrozek K., Sill H., Knuutila S., Kolitz J.B., Archer K.J.,

Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;

"BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia.";

Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
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01-MAR-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
BAALC 1-5-6-8.
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Mammalia; Eutheria;
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Mammalia; Eutheria;
NCBI_TaxID=9823;
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                                                                                                                                EQUENCE FROM N.A.

CSTRAIN=C57BL/61; TISUE=Whole body;

CSTRAIN=C57BL/61; TISUE=Whole body;

X MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

X MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

A Shibate K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

A Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,

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A Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,

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T sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
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STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carrinci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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01-JUN-2001
01-JUN-2001
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STRAIN=C57BL/60; TISSUE=Whole body;
MEDLINE=20499374; pubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs t
prepare full-length cDNA libraries for rapid discovery of new
Genome Res. 10:1617-1630(2000).
                                                 SEQUENCE FROM N.P
STRAIN=C57BL/6J;
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STRAIN=C57BL/6J; TISSU
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2810457D07 product:brain and acute leukemia,
cytoplasmic, full insert sequence.
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STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=21085660; PubMed=11217851;
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                     Akimura
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01-MAR-2002
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAR-2002 (TrEMBLrel.
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BAALC 1-5-6-7-8.
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Pred. No. 5.3e-37;
3; Mismatches 12
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Catarrhini;
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Best Local (
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MEDLINE=21574584; pubMed=11707601; DOI=10.1073/pnas.241525498;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinor Mrozek K., Sill H., Knuutlia S., Kolitz J.E., Archer K.J.,

Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;

"BAALC, the human member of a novel mammalian neuroectoderm ge lineage, is implicated in hematopoiesis and acute leukemia.";

Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).

EMBL, AF371325; AAL50521.1, -.

InterProc. IPR009728; BAALC_N.
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MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinoner

Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,

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"BAALC, the human member of a novel memmalian neuroectoderm gene
lineage, is implicated in hematopoiesis and acute leukemia.";

Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
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05-JUL-2004
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01-MAR-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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Eukaryota; Metazoa; Chordata;
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Mammalia; Eutheria;
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NCE 54 AA; 5667 MW;
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                                          MGCGGSRADAIEPRYYESWTRETESTWLTYTDSDALPSAAATDSGPEAGGLHAG
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Sciurognathi; Muridae; Murinae; Rattus.
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QBWXSD
ID QBWXS
AC QBWXS
AC QBWXS
DT 01-MA
TO ZEC
RA MIOZE
RA MIOZE
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RA MIOZE
RA MIOZE
RA Calig
RA T11inee
RA Pfan;
DR EMBI;
DR EMBI;
DR EMBI;
DR EMBI;
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Q8WTP6
ID Q8WTP
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Best Local S
Matches 53
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

PROBLINE-21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;

MEDLINE-21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen Mrozek K., Sill H., Kruuutila S., KOlitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;

"BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia.";

Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).

EMBL; AF365578; AAL50380.1; -.

Pfam; PF06589; BAALC N; 1.

SEQUENCE 73 AA; 7871 MW; 98DBC2E6E6EF524A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

PubMed=11707601; DOI=10.1073/pnas.241525498;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen Mrozek K., Sill H., Knuuttila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;

"BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia.";

Proc. Nati. Acad. Sci. U.S.A. 98:13901-13906(2001).
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Q8WTP6;
Q1-MAR-2002
01-MAR-2002
05-JUL-2004
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Q8WXS0;
01-MAR-2002
01-MAR-2002
           Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergran E.J., LU X., Gibbs R.A.,
Paher, J. Halton E. Ketteman M. Madan A. Roditiones S. Sanchez A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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2 (TrEMBLrel.
4 (TrEMBLrel.
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(TrEMBLrel.
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Primates;
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    Last sequence update)
    Last annotation update)
    protein) (BAALC 1-8).

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Catarrhini;
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.8e-20;
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RESULT
Q8WNE8
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DT 01
DT 01
DT 01
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Best Local S
Matches 50
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Best Local Similarity
Matches 51; Conserv
                         Q8WNE8
Q8WNE8;
Q8WNE8;
O1-MAR-2002 (TrEMBLrel.:
O1-MAR-2002 (TrEMBLrel.:
O1-MAR-2004 (TrEMBLrel.:
BAALC isoform 1-8.
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Q8WXS2;
Q1-MAR-2002
01-MAR-2002
01-MAR-2004
                                                                                                                                                                                                                                              MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498; Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinoner Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.; "BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia."; Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).

EMBL; AF363578; AAL50382.1; -.
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Submitted (JUL-2002) to the EMI
Submitted (JUL-2002) to the EMI
EMBL; AF371323; AAL50519.1; -.
EMBL; BC035038; AAL50378.1; -.
EMBL; AF363578; AAL50378.1; -.
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Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., But
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A.,
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF06989;
SEQUENCE 54 1
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TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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    scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                              sapiens (Human)
                                                                                                                                                                  μ.
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(TrEMBLrel.
                                                                                                                                                                                        35.5%; ilarity 94.3%; Conservative
                                                                                    PRELIMINARY;
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AA; 8573
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AA; 5663 MW;
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Primates;
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                                                                                                                                                                                                                                       MW.
                                     20,
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1; Mismatches
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Last
                                     Last sequence update)
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                                                            Created)
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annotation update)
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i; Hominidae;
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; Homo.
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A., Schein J.
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З.
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Eukaryota; Alveolata;

Apicomplexa;

Haemosporida;

Plasmodium binding

precursor sequence up

(Erythrocyte

Duffy receptor, alpha

19, 34, 43,

Last Last form

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MEDLINE=92357776; SEQUENCE FROM N. NCBI_TaxID=5850; Plasmodium

PubMed=1496004;

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RESULT 14
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QB01V5
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AC QB01V
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DT 01-JI
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01-AUG-1991 (Rel.
01-OCT-1996 (Rel.
29-MAR-2004 (Rel.
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NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
NCBI TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                    PVDA PLAKN
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MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;

MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;

Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinor Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,

Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,

Caligiuri M.A., Bloomfield C.D., de la Chappelle A.,

Caligiuri M.A., Bloomfield C.D., de la Chappelle A.,
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Mammalia; Eutheria;
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Pred. No. 3.4e-08;
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"The Duffy receptor family of Plasmodium knowlesi is located within the micronenes of invasive malaria merozoites.";

Cell 63:141-153(1990).
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EMBL; M68517; AAA29590.1; -.
EMBL; M68518; AAA29591.1; -.
PIR; A35970; A35970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 296-1073 FROM N.A. MEDLINE-91004213; PubMed=2170017; DOI=10.1016/0092-8674(90)90295-P; Adams J.H., Hudson D.E., Torii M., Ward G.E., Wellems T.E., Alkawa M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
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13; Mismatches
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N-linked
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Duffy receptor, alpha form.

Extracellular (Potential).
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